

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 05:47:40 ; Search time 1870.66 Seconds
(without alignments)
14318.993 Million cell updates/sec

Title: US-09-970-624-1
Perfect score: 1280
Sequence: 1 gccacgagccgccccgcgcca.....aaaaaaaaaaaaaaaaaaaa

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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Result No.	Score	Query Match Length	ID	Description
1	1109.6	86.7	1268	6 AX085151
2	1109.6	86.7	1268	6 AX085348
3	1109.6	86.7	1268	6 AF112149
4	463.4	36.2	5031	6 AX085162
5	463.4	36.2	5031	6 AX085359
6	290	22.7	936	6 AMDEPH125
7	265.6	20.8	687	6 AF336979
8	254.8	19.9	775	6 MSU91964
9	249.6	19.5	916	6 AF312662
10	245	19.1	310	6 AX085160
11	245	19.1	310	6 AX085357
12	239.4	18.7	1098	6 ATANR1
13	236.4	18.5	801	6 ATU20186
14	208.6	16.3	1039	6 AF396746
15	176.8	13.8	1061	6 AF099937
16	174.4	13.6	251	6 AX085161
17	174.4	13.6	251	6 AX085358
18	172.8	13.5	1355	6 PMU69483
19	172.8	13.5	1642	6 PMU46582
20	172.8	13.5	1726	6 AF006210
21	171.2	13.4	922	6 AF023615
22	171.2	13.4	1657	6 PMU69482
23	171.2	13.4	1753	6 PADAL2
24	167.6	13.1	1212	6 PMU69484
25	165.8	13.0	1009	6 AF234617
26	165.8	13.0	1043	6 AR088956
27	165.8	13.0	1043	6 OSU78782
28	165.2	12.9	1069	6 ZMU31522
29	164.8	12.9	1154	6 GGN132209
30	163.4	12.8	1037	6 MDO25118
31	161	12.6	1351	6 MEZAC1A
32	159.8	12.5	174264	2 OSJN00003
33	159.4	12.5	1080	6 PGORFAG2
34	158.4	12.4	984	6 HVO249145
35	158.4	12.4	999	6 PHEBP11
36	157.6	12.3	1262	8 MEZMAPSA
37	157.2	12.1	1175	8 AB003324
38	155	12.1	861	8 HVO249142
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43	151	11.8	1176	8 AB007505
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45	150.6	11.8	1193	8 AF151693

ALIGNMENTS

Result No.	Score	Query Match Length	ID	Description
1	1109.6	86.7	1268	6 AX085151
2	1109.6	86.7	1268	6 AX085348
3	1109.6	86.7	1268	6 AF112149
4	463.4	36.2	5031	6 AX085162
5	463.4	36.2	5031	6 AX085359
6	290	22.7	936	6 AMDEPH125
7	265.6	20.8	687	6 AF336979
8	254.8	19.9	775	6 MSU91964
9	249.6	19.5	916	6 AF312662
10	245	19.1	310	6 AX085160
11	245	19.1	310	6 AX085357
12	239.4	18.7	1098	6 ATANR1
13	236.4	18.5	801	6 ATU20186
14	208.6	16.3	1039	6 AF396746
15	176.8	13.8	1061	6 AF099937
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18	172.8	13.5	1355	6 PMU69483
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30	163.4	12.8	1037	6 MDO25118
31	161	12.6	1351	6 MEZAC1A
32	159.8	12.5	174264	2 OSJN00003
33	159.4	12.5	1080	6 PGORFAG2
34	158.4	12.4	984	6 HVO249145
35	158.4	12.4	999	6 PHEBP11
36	157.6	12.3	1262	8 MEZMAPSA
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38	155	12.1	861	8 HVO249142
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40	152.4	11.9	1039	8 ZMA271208
41	151.6	11.8	1170	8 GGN132207
42	151.4	11.8	1095	8 AB003328
43	151	11.8	1176	8 AB007505
44	150.8	11.8	1083	8 ZMU31521
45	150.6	11.8	1193	8 AF151693

RESULT 1
LOCUS AX085151 1268 bp DNA linear PAT 09-MAR-2001
SEQUENCE AX085151 Sequence 1 from Patent WO0112798.
ACCESSION AX085151
VERSION AX085151.1 GI:13275244
KEYWORDS
SOURCE
ORGANISM Zea mays.
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1268)
Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
Male sterile plants
Patent: WO 0112798-A 1 22-FEB-2001;
Suedwestdeutsche Saatzeugs (DS)
JOURNAL Location/Qualifiers
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Db	474	AGTTATGATTCGCGTACGGCAAGCCCAAGGAAGAGCAGCAAGTGTGGCAAAATGCCAACTC	533
Qy	611	ggagcttaaatcttggcaaaaggagagcaagaactcttggagcaacaactctgacaacttgc	670
Db	534	GGACCTTAAGCTTTGGCAAAAGGGGCGACGACAGACTTTGACCAACACTGCACAACTTGC	593
Qy	671	agaaatattcgcgcagcttgcacggagatga tcttctcgtggctgaatgtcaaaagctgc	730
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Db	654	GTCCCTGGAGATCAATCAATTTGGAACAAACCCCTGCGGTGTCGGCGCAAGAAGGACATCT	713
Qy	791	cttatagatgagatctcaagatcttgcacgcgaagcgcaagttaattccacaagaanaat	850
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Db	774	AGACTTTGACAAATGAAGATCAACCTGATTCGCCAAGAAATGATGATGTACATAAAGAT	833
Qy	911	ataagaagcttgaagaccgaatggagttaatctggagatcaaccgcatccatcaacttgc	970
Db	834	CTATGACACTTAAGAGCACAATGSGAGTTTAATCGGAGTCACCGACTTCATTTCACTTGC	893
Qy	971	agtagtagaanaaccagagatgtctctgttgcacacttgaactagacacactgcacagcaaa	1030
Db	894	AGTAGTAGAANAACCAGAGATGTTCAGTAGTCAACTGAACTCGACACACTCGCACAAACAA	953
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Qy	1091	aaactgcgcgtctatga tgcctgaagaagaactatttacttggagaagatga tactcag	1150
Db	1014	AAAACCTGCCGCTTATGATGCTGGAAGGAACATTTATTTGGAAGAGATGATCTACAG	1073
Qy	1151	aaagacatatttggcgscggagagatttgaagatagaactataatgtgaatgcaataat	1210
Db	1074	AAAGACATATTTGTGCGCAGGCGAGATTGAGATATTAACCTTTAAATGTAAATGCAAA	1133
Qy	1211	tttcgaccggaatgggctgtggaattccaagatga tga tttcttcta	1258
Db	1134	TTTTCAGACTGGAATGGCGTCTGGAATTCAGAGATGATTTGCTTTCTA	1181
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DEFINITION	Zea mays MADS box protein 2 (mads2) mRNA, complete cds.		
ACCESSION	AF112149		
VERSION	AF112149.1	GI:9964295	
KEYWORDS			
SOURCE			
ORGANISM			
	Zea mays.		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC		
	clade; Panicoideae; Andropogoneae; Zea.		
	1 (bases 1 to 1268)		
REFERENCE			
AUTHORS	Heuer, S., Loerz, H. and Dresselhaus, T.		
TITLE	The MADS box gene ZmMADS2 is specifically expressed in maize pollen		
JOURNAL	and during maize pollen tube growth		
REFERENCE	Sex. Plant Reprod. 13, 21-27 (2000)		
AUTHORS	2 (bases 1 to 1268)		
	Heuer, S., Dresselhaus, T. and Loerz, H.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-DEC-1998) Centre for Applied Molecular Plant Biology		

						FEATURES	
						source	
AMP II, University of Hamburg, Ohnhorststrasse 18, Hamburg 22609, Germany							
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Matches 1166;	Conservative	0;	Mismatches 14;	Indels	8;	Gaps	4.
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Db	1	TCGCGCTACGCTTCCTC--CTCTCTCCCTCCTTGTCTTCTTCTTCTTCTTCTTGC	58				
Oy	131	ggaaacctgtcgccttttgagcttcttcttcttgagagctcccacagaattcctcctcctt	190				
Db	59	GGAAACCTGCTGCCCTTTGAGACTTCTTCTTCGATGCTCCACCACAATCTCCCTCCCTT	118				
Oy	191	accctcttggcaagcttcgagcgcgcgcgcgaggaaagtatagatccggcatctgctg	250				
Db	119	ACCTTCTTTGGCACGTTTCGGCGCGCGCGGGAGATGATGATCCGCCATCGTGTGCG	178				
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Db	179	-CGGTCTTGTCTTCGATCGGAGGCGCACACCAACAACCTCTGCTTAGCGTGCGCG	237				
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Oy	371	aaaagatcgatgataccgaagatcgatatcactcaagagccggcgaagtgaaccttccaagc	430				
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Oy	491	ctctgcatcattctcgaagcacggcgcgctctacagtatctttagcaacgcgatgaatc	550				
Db	414	CTCTGTCATCTTCCACGACACCGGCCCTCTACGATCTACTTACGACCCAGCATGAATC	473				
Oy	551	agtatagatcgcgtagcagcgcaagggcaagagaagcaagtcgtgcaatccccaatc	610				
Db	474	AGTATAGATCGGTACGGCAAGGCGCAAGAGAGACACCAAGTCTGTCCAAATGCCAACCTC	533				
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LOCUS AX085162
DEFINITION Sequence 12 from Patent WO0112798.
ACCESSION AX085162
VERSION AX085162.1 GI:13275254
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 5031)
Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
Male Sterile Plants
Patent: WO 0112798-A 12 22-FEB-2001;
Suedwestdeutsche SaatZucht (DE)
Location/Qualifiers
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Best Local Similarity 96.5%; Pred. No. 1.4e-96;
Matches 518; Conservative 0; Mismatches 11; Indels 8; Gaps 4;

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RESULT 5
AX085359 5031 bp DNA linear PAT 09-MAR-2001
LOCUS AX085359
DEFINITION Sequence 12 from Patent WO0112799.
ACCESSION AX085359
VERSION AX085359.1 GI:13275414
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 5031)
Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
Regulatory sequences for pollen specific or pollen abundant gene
expression in plants
Patent: WO 0112799-A 12 22-FEB-2001;
Suedwestdeutsche SaatZucht (DE)
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RESULT 7
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 LOCUS Arabidopsis thaliana MADS-box protein AGL21 mRNA, complete cds.
 DEFINITION AF336979
 ACCESSION AF336979.1 GI:18478602
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 KEYWORDS
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 ORGANISM Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 687)
 AUTHORS Burgeff,C., Liljegren,S.J., Yanofsky,M.F. and Alvarez-Buylla,E.R.
 TITLE MADS-box gene expression in lateral primordia, apical meristems and
 differentiated tissues of Arabidopsis thaliana roots
 JOURNAL 2 (bases 1 to 687)
 REFERENCE Burgeff,C., Liljegren,S.J., Yanofsky,M.F. and Alvarez-Buylla,E.R.
 AUTHORS Direct Submission
 TITLE Submitted (15-JAN-2001) Lab. Genetica Molecular y Evolucion,
 Instituto de Ecologia, UNAM, Tercer Circuito Exterior, Anexo al
 Jardin Botanico, Mexico City, DF 04510, Mexico
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BASE COUNT 245 a 136 c 154 g 152 t
 ORIGIN

Query Match 20.8%; Score 265.6; DB 8; Length 687;
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 Oy 420 ttctccaagcgccggaagatcttccaagagcgcaagagctgcctactctcgact 479
 Db 61 TTCTCCAAACGAGAAAGGCTTATCAAGAAAGCCAAAGACTAGCTAATTCCTGTGAT 120
 Oy 480 gggagagtcgcgcctgcactcttccacagcagcgccgcctctacgaactctagacc 539
 Db 121 GCCGAGTCGCGTCTCATCATCTTCTCTGACACCGGAAAGCTCTATGACTTTGGCAAGTCC 180
 Oy 540 agcaggaatcagttatagatcgtacgagcagcgcaaggaagagcagcagtcgtcgca 599
 Db 181 ACCATGAAGTCGTTATGATAGATACCAAGCAAGATCGAGACACCAACTATTG 240

Oy 600 aatcccaactcggagcttaagtgttgcaaaagggagcgagcaagcttgagacaactg 659
 Db 241 AACCCCGCATCAGAGTCAAGTTTGGCAGAGAGAGCTGCTTCTTAAGCAAGAACTG 300
 Oy 660 cacaactcgaagaatlatcggcagcttgacggagagatgactcttcctggcgtgaagtc 719
 Db 301 CATGCTTTGGCAAGAAATCATCGGCAATTCATGATGGAGACAGCTTAATGTTAAGTGT 360
 Oy 720 aagaactgcagctccctggagaaatcaaltggaacaagcctgcgtgltgcgcgcaag 779
 Db 361 AACGAGCTTAACAGTCTTGAGAAATCAAAATGAGATTAAGTTGCGTGAATTCATGAGA 420
 Oy 780 aagagccctctctatagatgagatcagattgaaatgaaagggcaagttatctcac 839
 Db 421 AAGGAACAACCTTGACTCAAGAAATCCAGAACTAGCCAAAGAGCAATCTTAATTCAT 480
 Oy 840 caagaanaatacagactgtacataagaatcaactgtatgcgaagaanaatgagtgta 899
 Db 481 CAGGAACAACCTGATTTATTCAGAAAGTACACGGAATTCATCAAGAAATGTGAGCTC 540
 Oy 900 cataaagaatataatgagac 919
 Db 541 TACAAGAAAGCTTATATGCG 560

RESULT 8
 MSU91964 775 bp mRNA linear PLN 05-APR-1997
 LOCUS Medicago sativa MADS-box protein mRNA, partial cds.
 DEFINITION MSU91964
 ACCESSION U91964
 VERSION U91964.1 GI:1928873
 KEYWORDS
 SOURCE Medicago sativa.
 ORGANISM Medicago sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 REFERENCE 1 (bases 1 to 775)
 AUTHORS Dunn,K. and Heard,J.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-1997) Biology, Boston College, 140 Commonwealth
 Ave, Chestnut Hill, MA 02167, USA
 FEATURES
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 /protein_id="AB51377.1"
 /db_xref="GI:1928874"
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BASE COUNT 283 a 128 c 179 g 185 t
 ORIGIN

Query Match 19.9%; Score 254.8; DB 8; Length 775;
 Best Local Similarity 69.0%; Pred. No. 1.9e-48;
 Matches 349; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Oy 366 aggggaagatcgtatccgcagagatgaactccacgagcgagtgagactctcc 425
 Db 1 AGAGGGAAGATTCAGATTAAGAGATGAGACACAAAGCAAGCAAGTAACTTTTTCG 60
 Oy 426 aagcgccggaagcgagatcttcaagaagcgcaagagagctgcacactctgcatcgag 485

Db	61	AAGCGAAGATATGATTTGTTGAGNAGCGGAGAACCTGGATTTTGTGATGCTGAG	120
QY	486	gtcggcctcgcatacttctccaagcaccggccgctctacgaagtlactagaccagcatg	545
Db	121	GTTGGGGTTATGATCTTCTCCAGCAGCTGCAAAACCTCTATGATTTGGCCAGCACCGTTG	180
QY	546	aaatcagttatagatcagtlacgcgcaaggccaagbaaagacgacgaagtcgtgcgaattcc	605
Db	181	AGATCAGTAATTTGGTAGATATPACAAATCAAAAGAGAACATTAATCAACTTGGGGGTGCA	240
QY	606	aactcggagcttaagtttttgcgaagggagcagaagaagcttgaagacaacaactgcacac	665
Db	241	GCCTTGAAATTTAACTTTGGGCAAAAGGAGGACAGTGTTAAGGCAACAAATTGCACAT	300
QY	666	ttgcagaagaanaattacgcgcagttgcagggagatgatcttcttggctgaatgcacaaga	725
Db	301	CTCGAMGAAGTCAACCGGCAATATGGGTGAGAAATTATCAGGTTTACAGTCAACAA	360
QY	726	ctgcagtccttcgagaaatcaattggaacaagcctgcgtgctgcgcgcaagaagaagac	785
Db	361	TTACAGGGTTTGGAGAACCAATTTGGAATTCAGCTTCTCGTGTTCGTATCAAAAAGGAC	420
QY	786	catctcttgatagatlgaaatccaogatttgaatcgaagaagcaagtttatcttccacaaga	845
Db	421	CAACTTTTATGATGAAGAAATCAAAACAACTAAATCGAAAGGGGACATTTCCACCAAGA	480
QY	846	aatacagacttgatacaataagaatca 871	
Db	481	AATGTCGAAGCTGATCGTAAGGTCTA 506	

RESULT	9
AF312662	
LOCUS	916 bp mRNA linear PLN 04-MAY-2001
DEFINITION	Arabidopsis thaliana MADS-box protein AGL16 (AGL16) mRNA, partial cds.
ACCESSION	AF312662
VERSION	AF312662.1 GI:1154538
KEYWORDS	.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 916)
AUTHORS	Alvarez-Buylla,E.R., Liljgren,S.J., Pelaz,S., Gold,S.E., Buergeff,C., Ditta,G.S., Vergara-Silva,F. and Yanofsky,M.F.
TITLE	MDS-box gene evolution beyond flowers: expression in pollen, endosperm, guard cells, roots and trichomes
JOURNAL	Plant J. 24 (4), 457-466 (2000)
MEDLINE	20566573
PUBMED	1115127
REFERENCE	2 (bases 1 to 916)
AUTHORS	Liljgren,S.J. and Yanofsky,M.F.
TITLE	Direct Submission
JOURNAL	Submitted (12-OCT-2000) Biology, University of California at San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0116, USA
FEATURES	location/Qualifiers
source	1..916

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<1..655
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/protein_id="AA037889.1"
/db_xref="GI:11545539"

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BASE COUNT	293 a	193 c	194 g	296 t
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Query Match	19.5%	Score 249.6	DB 8	Length 916
Best Local Similarity	63.2%	Pred. No. 3e-47		
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Db	1	GGGAAGAAATGATGATTGTTGAAAGAAAGCTTAAGAGGCTTCGATTTCTCTCGATGCTGAGGT	60
OY	488	cggcctctgcatctctccacgaccgcgcgcctctcagatctactagaccagatgaa	547
Db	61	TGGTGTCAATCATCTTCTCCAGCAGCGGTAAAGGCTTACGATTTCTCCAGCTCAGCATGAA	120
OY	548	atcagttatagatcggatcgcgcaaggcccaaggaagagcagcagaatcgctcgcaaatcccaa	607
Db	121	ATCGGTGCATATAGAGAAATACAGAGCATGCCAAGGGGAAACCAAGTTGCAAAATATGATCCGC	180
OY	608	ctcggagcttaagcttttgcaagaagagcagcaagctctgagacacacactgcacactg	667
Db	181	TTTCAGAAATTTCAAGTTCTTGCGCAAAAGGAGGCTTCGATTTCTAAAGCTGACGTACATACTT	240
OY	668	gcaagaaataatcgcgcagcttgacggagagatgaltcttctggtcgtgaatgltcaagaact	727
Db	241	GCAAGAAAAACCCCGGCAAAATGATGGGGAGAGGACTCTCTGGACTAAAGTGTGAAGCTTT	300
OY	728	gcagtcctctggagaatcaatctggaacaagcctctggtgtgtgtctcgcgcaagaagagacca	787
Db	301	ACAGAAATTTGGAAATACAGCTTGAATTAAGCTTGTGTGGCGTTGCAATGAAGAAAGATCA	360
OY	788	tcctcttgatagatgagatccaagatcttgaatcgaaagccaagttatcttaccacaagaaa	847
Db	361	AATGTTAATTCGAAGAAATATACAAAGTACTTAACCGAAGGGGAATCTCGTTACCAAGAGAA	420
OY	848	tacgaactctgtacaataagaatcaacctctgatctcgccaagaanaatgtatgattacataaaa	907
Db	421	TTTAAACCTCCCAAGAAATGAAACCTAATGACCCACCAAGAACATGACATACATGAAGAA	480
OY	908	gatatatagactgaagaagcaacgaagtggaggttaatcoggagatcaacgactccaataactt	967
Db	481	GGTTTCAAGAGCTCGAGGGGTGTCAAAATGCGCAACAAAGAAATTTCTTTCTCACCAATATGCTT	540
OY	968	tgcagttatagaaaacagagatgltctctgtgcaacttgaactcaagcacactgccaagca	1027
Db	541	AGACATGTAGAGATTAACCTCGAAGCAACATGTCCATCTTCAGCTCAGCCCAACCGCACATGA	600
OY	1028	aatataca 1035	
Db	601	TCATGAGA 608	

RESULT	10			
AX085160				
LOCUS	AX085160	310 bp	DNA	linear
DEFINITION	Sequence	10 from Patent WO0112798.		PAT 09-MAR-2001
ACCESSION	AX085160			
VERSION	AX085160.1	GI:13275252		
KEYWORDS	.			
SOURCE	Zea mays.			
ORGANISM	Zea mays.			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC			
	clade; Panicoideae; Andropogoneae; Zea.			
	1 (bases 1 to 310)			
REFERENCE	Loerz,H., Dresselhaus,T., Schneider,D. and Heuer,S.			
AUTHORS	Mate sterile plants			
TITLE	Patent: WO 0112798-A 10 22-FEB-2001;			
JOURNAL				

FEATURES
source
Suedwestdeutsche Saatztucht (DE)
Location/Qualifiers
1. .310
/organism="Zea mays"
/db_xref="taxon:4577"
BASE COUNT 51 a 112 c 68 g 79 t
ORIGIN

Query Match 19.1%; Score 245; DB 6; Length 310;
Best Local Similarity 95.3%; Pred. No. 3.1e-46;
Matches 285; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

OY 44 aaacgcacacataagaatcatcctccctcgcgcgtacgtcttccctcctccctcct 103
Db 1 AAACGCACACATAGAGATCATTCCTCCCTCGGCTACCTCTCCCTCCT 58
OY 104 cctccctctctc-ttccctcctcttggaacctcgtcgtcttgagcttctctc 162
Db 59 CTGCTCTTCT 118
OY 163 agagctccacacagatctcctcctccttactcttcttgagcgtctgagcgcg 222
Db 119 AGTGTCTCCACAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
OY 223 aagaagatagatccgcgcacatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 282
Db 179 AGATAGATAGATCCCGCATCTGCTGTC-CGCTCTCTCTCTCTCTCTCTCT 237
OY 283 cacaacctctcgtccatagcgtgcaagcgagcgaggtcaagaagaagctagcta 341
Db 238 CACAACCT 296

RESULT 11
AX085357
LOCUS AX085357 310 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 10 from Patent WO112799.
ACCESSION AX085357
VERSION AX085357.1 GI:13275412
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
Regulatory sequences for pollen specific or pollen abundant gene
expression in plants
Patent: WO 0112799-A 10 22-FEB-2001;
JOURNAL
Suedwestdeutsche Saatztucht (DE)
FEATURES
Location/Qualifiers
1. .310
/organism="Zea mays"
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BASE COUNT 51 a 112 c 68 g 79 t
ORIGIN

Query Match 19.1%; Score 245; DB 6; Length 310;
Best Local Similarity 95.3%; Pred. No. 3.1e-46;
Matches 285; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

OY 44 aaacgcacacataagaatcatcctccctcgcgcgtacgtcttccctcctccctcct 103
Db 1 AAACGCACACATAGAGATCATTCCTCCCTCGGCTACCTCTCCCTCCT 58
OY 104 cctccctctctc-ttccctcctcttggaacctcgtcgtcttgagcttctctc 162
Db 59 CTGCTCTTCT 118
OY 163 agagctccacacagatctcctcctccttactcttcttgagcgtctgagcgcg 222

Db 119 AGTGTCTCCACAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
OY 223 aagaagatagatccgcgcacatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 282
Db 179 AGATAGATAGATCCCGCATCTGCTGTC-CGCTCTCTCTCTCTCTCTCTCT 237
OY 283 cacaacctctcgtccatagcgtgcaagcgagcgaggtcaagaagaagctagcta 341
Db 238 CACAACCT 296

RESULT 12
ATANR1
LOCUS ATANR1 1098 bp mRNA linear PLN 11-MAR-1998
DEFINITION Arabidopsis thaliana mRNA for MADS-box transcription factor.
ACCESSION 297057
VERSION 297057.1 GI:2959319
KEYWORDS
SOURCE
MADS-box; transcription factor.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
Autors
Forde,B.G.
JOURNAL
Submitted (18-JUN-1997) Forde B.G., Biochemistry and Physiology
Department, IACR-Rothamsted, Harpenden Herts AL5 2JQ UK
2 (bases 1 to 1098)
REFERENCE
Zhang,H. and Forde,B.G.
A Arabidopsis MADS box gene that controls nutrient-induced changes
in root architecture
Science 279 (5349), 407-409 (1998)
JOURNAL
Science 279 (5349), 407-409 (1998)
MEDLINE
98092528
FEATURES
source
Location/Qualifiers
1. .1098
/organism="Arabidopsis thaliana"
/isolate="Landsberg erecta (Ler)"
/db_xref="taxon:3702"
97. .801
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BASE COUNT 397 a 190 c 216 g 295 t
ORIGIN

Query Match 18.7%; Score 239.4; DB 8; Length 1098;
Best Local Similarity 63.9%; Pred. No. 7e-45;
Matches 379; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

OY 352 ggaagatcagtgaggagaaagatcgtatccgcagagatataatccacagcg 411
Db 89 GGAGAGAGATGGGAGAGAGAGAGATAGTATACGAAGATTCATCTACAAATAGAC 148
OY 412 agttagactctccaaagcgcggaagcgtctcaagaagcgcaagagcgtccatcc 471
Db 149 AAGTAGCTTCTCCCAAGAGAGAGAGAGGTTGCTTAAAGAGCTTAAGAGTTATGATCC 208
OY 472 tctgagatgcgagagtcgagcctcgtcatctctccagacgagcgagcgtctagtgat 531

Db	209	TTTGTGATGCAGAGAGTTGGTGTTATCTATCTTCTAGCACCGGAAGCTCTACGACTACG	268		
Qy	532	ctagca---ccagatgtgaatcagtlataagtcgtaacgycgaagccaggaagagcagc	588		
Db	269	CAACGCAATTCAAAGTATGAAAAACATCATTTGAGCGGTCAACAGAGTAAAGAGAGCAGC	328		
Qy	589	aagtcgctgcaaatcccaactcggaagttgaagtttggcaagagagagcaagcttga	648		
Db	329	ATCAACTCTTGAAATCATGCGCTCAGAGATTAAGTTTGGCAAGAGAGGTTGCAGATTTCG	388		
Qy	649	gacacacactgcaacaactctgcaagaaatlatcgacagcttgaacggaatgatcttcg	708		
Db	389	AGCAGCAGCTCCACATCTCAAGAAATGCCACAGAAACTAGTGGAGAGAACTTCTCG	448		
Qy	709	gagctgaatgtcaaaagaactcagtcagtcacctggaagaatcaattggaacaagcctgctgtg	768		
Db	449	GAATGATGCTTAACGACCTTACMAAATCTTGAAAGCCAGCTAAGTAAAGCTTAAAGGTG	508		
Qy	769	tcgcgcgaagaagaagaccatctctgtgtagatgagatcacaagatlttaalcgaagycaa	828		
Db	509	TTCTGCTTCACAAAAGAGATCAACTTATGACAAATGAAATCAGAGAACTTAATGTAAGGAC	568		
Qy	829	gttatttcaccaaagaatcacagactgttaacataagatcaaccttatttcgccaagaa	888		
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Db	629	ATATTAAATTGCAAAAGAGAGTTTCATGAGAACACAAATGTGATTCGAAGCAAT	681		
RESULT 13					
LOCUS	ATU20186	801 bp	mRNA linear PLN 22-OCT-1995		
DEFINITION	Arabidopsis thaliana MADS-box protein AGL17 (AGL17) mRNA, partial cds.				
ACCESSION	U20186				
VERSION	U20186.1	GI:862647			
KEYWORDS	.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.				
REFERENCE	1 (bases 1 to 801)				
AUTHORS	Rounsley,S.D., Ditta,G.S. and Yanofsky,M.F.				
JOURNAL	Diverse roles for MADS box genes in Arabidopsis development				
MEDLINE	Plant Cell 7 (8), 1259-1269 (1995)				
REFERENCE	96004530				
AUTHORS	2 (bases 1 to 801)				
TITLE	Purugganan,M.D., Rounsley,S.D., Schmidt,R.J. and Yanofsky,M.F.				
JOURNAL	Molecular evolution of flower development: diversification of the				
MEDLINE	plant MADS-box regulatory gene family				
REFERENCE	Genetics 140 (1), 345-356 (1995)				
AUTHORS	95362031				
TITLE	3 (bases 1 to 801)				
JOURNAL	Rounsley,S.D.				
MEDLINE	Direct Submission				
REFERENCE	Submitted (23-JAN-1995) Steven D. Rounsley, Biology-0116,				
AUTHORS	University of California at San Diego, La Jolla, CA 92093-0116, USA				
TITLE	Location/Qualifiers				
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CDS					

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Db	1	GATCCGAGAGAGATGATTCATCAACGAGTAGACAAATCCTTTCTCCAAAGCAAAAGG	60																								
Oy	440	gattcccaagaagcgaagagagctgcacatcctctcgaalgcggaagtcgcgcctgcat	499																								
Db	61	TCTCATCAAGAAAGCTTAAGAACTTGTAATCTTGCCAGCCGACGCTCTCTCATCAT	120																								
Oy	500	ctctctccagccgcgcgcctctcgaagtaactctctcgaacccgcagctgaaatcagttatga	559																								
Db	121	TTTTCTCCAAACATGACAAAGCTCTATGACTTTGCCAGCTCCAGTGTGAATCTTACTATTGA	180																								
Oy	560	tccgtagcagcgaagcgaagagcaagacgaatcgtcgcgaatcccaatcccaatccgaactaa	619																								
Db	181	ACGATTTCATACGGCTAGATGAGAGACAGCAAGAACTAATGAACCTGCATCAGAAAGTTAA	240																								
Oy	620	gttttcgcaaaaggagcgaacagctctgaagacacaaactgcacaactctgcaagaataa	679																								
Db	241	GTTTTGGCGAGAGAGGCGCTGAACCTTAAGGCAAGAAATTCGATCTTTCGAAAGAAATTA	300																								
Oy	680	tccggaagttagcagagatgatcctctctcgggctgaatctcaagaactgcagtcgcctgga	739																								
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Oy	740	gaatcaattggaacaagagcctgcgtggtgtccgcgcaagaagagacatctctgtataga	799																								
Db	361	GAGTCMAATTTGAATGAGTTACGTGGGAATTCGTATGAAAAGGGAACAAATTTTACCAA	420																								
Oy	800	tgagatctcagatttgaatcgaagaagcaagttattctcgaagaataataacagactgtta	859																								
Db	421	TGAAATTTAAAGAGCTAACCAAGAAAGGAGATCTTGTTGATCTATGAAAACCTTGAAATTTGTC	480																								
Oy	860	caataagatcaacctgatctgcgcaagaanaaialgatgataaanaaatalatgagac	919																								
Db	481	GAGAAAGATGACAAAGATTCATCAACAAATGTCGAATATACAGAAGAGCTTATGGAAC	540																								
Oy	920	tgaaggaccaagtgaagt	937																								
Db	541	GTCGAACACAAATGGAAT	558																								
RESULT	14																										
AF396746																											
LOCUS	AF396746																										
DEFINITION	Ipomoea batatas MADS-box protein (MAUS1) mRNA, complete cds.																										
ACCESSION	AF396746																										

Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
 1 (bases 1 to 1039)
 Haung, Y.-S. and Yeh, K.-W.
 Cloning and characterization of a full-length cDNA encoding a
 MADS-box protein from sweet potato

JOURNAL
 Unpublished
 2 (bases 1 to 1039)
 Haung, Y.-S. and Yeh, K.-W.
 Direct Submission
 Submitted (02-JUN-2001) Botany, National Taiwan University, No.1,
 Sec.4, Roosevelt Rd., Taipei, Taiwan 106, Republic of China

FEATURES
 Location/Qualifiers
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 LMIFSTGKILHERATISIRSVIERYNKQDSQSLDPLLELQVIEVALIRLOLI
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 HOENFELFNFOAYGTSDPNAVNGDTISPYPDTISERSGSHIFQLPQNSDLRALY"

BASE COUNT 348 a 200 c 238 g 253 t
 ORIGIN

Query Match 16.3%; Score 208.6; DB 8; Length 1039;
 Best Local Similarity 64.6%; Pred. No. 9.2e-38;
 Matches 361; Conservative 0; Mismatches 189; Indels 9; Gaps 3;

QY 316 gccaggggtcaagaagagagctagctagctatagcgcgagatcgatggaggggaaaga 375
 DB 83 GACCAAGCTGCGAAGAACCCCATCCAGAAATAGGAGAGCAAGGATGGGAGGCAAGC 142
 QY 376 tcgtgatccgagatcgatactccacgagccgagcgagatcgatcccaagcgcgga 455
 DB 143 TTGAAATTAGGAGATGCAAAAGTCGACCAAGGACCAAGTCACCTTCTTGAAAGAGGAA 202
 QY 436 accggatcttcaagaagcgagagctcgccatctctcgatcgatcgagagtcgacctg 495
 DB 203 ATGGGTTGTGAAAGAGGCTATGAGATGGGATTTGTGCGATGCTGAAGTGGGATTGA 262
 QY 496 tcatctctccagacgagccgctctacgagatcttagcacagatgaatcaatga 555
 DB 263 TGATCTTCTCCAGCAGGAGAGCTCCATGATTCGACACACTAGCATCAGATCCGTTAA 322
 QY 556 tagatcgatcgcgaaagcgaaagaa---gcaagcaagtcgctcgcaatcccaactcg 612
 DB 323 TTGAACCTTACACACACACACAGGTGACAGCCCTTCATATCCCTCGAGACCAACATTAG 382
 QY 613 agcttaagctttggcaagggagggcagcagctttagaacaacaactgcgaacttgcag 672
 DB 383 AACCTCAAGTTTGGCAATATGAAAGTACCAATCTGAGGCAACAAATTACACATCATGCAAG 442
 QY 673 aaatttcgagcagttgacgagagatgattctctgctgagatgacgcaagacatcgact 732
 DB 443 AAGATCATCGGAAGTAAATGGAGAAC---TCTATGGGCTGAGTGTAAAGACTCTCAGA 499
 QY 733 cccctggaatcaattggaacaagcctgctgctgctcgcaagaagacatctctc 792
 DB 500 ATCTTGAACCAACGAGGAATGATTTGAGCGGCATGCAAGATGAGAGAGCAACAATAC 559
 QY 793 tgatagatgagatcagatattgaaatcgaa---aggcaagttattctcaccagaataa 849
 DB 560 TAATTTGAACAGATTCAAGAACTAACCCACAGCAGGAGGATTTCGTGCACACAGGAACACT 619

QY 850 caccatgtacaataagat 868
 DB 620 TTGAATCTTTAAATAGTT 638

RESULT 15
 AF099937
 LOCUS
 DEFINITION
 Hyacinthus orientalis AgAMOUS homolog transcription factor (HAG1)
 mRNA, complete cds.
 AF099937
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Hyacinthus orientalis.
 Hyacinthus orientalis.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 Hyacinthaceae; Hyacinthus.
 1 (bases 1 to 1061)
 Zhang, X.-S., Li, Q.-Z., and Li, X.-G.
 Regulation of HAG1 expression in the organogenesis system of
 Hyacinthus orientalis in vitro
 Unpublished
 2 (bases 1 to 1061)
 Li, Q.-Z., Zhang, X.-S., and Li, X.-G.
 Direct Submission
 Submitted (19-OCT-1998) College of Life Sciences, Shandong
 Agricultural University, Daizong, Taitan, Shandong 271018, P.R.
 China
 3 (bases 1 to 1061)
 Li, Q.-Z., Zhang, X.-S., and Li, X.-G.
 Direct Submission
 Submitted (25-MAY-1999) College of Life Sciences, Shandong
 Agricultural University, Daizong, Taitan, Shandong 271018, P.R.
 China

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

REMARK
 COMMENT
 FEATURES
 source
 Location/Qualifiers
 1..1061
 /organism="Hyacinthus orientalis"
 /db_xref="taxon:82025"
 1..1061
 /gene="HAG1"
 /note="flower identity gene"
 134..820
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 /codon_start=1
 /product="AGAMOUS homolog transcription factor"
 /protein_id="AADI9360.2"
 /db_xref="GI:4887234"
 /translation="MGRGKVEIRIKETSTNRVYFWKRNGLIKKAMENGILCDAEVG
 LMIFSTGKILHERATISIRSVIERYNKQDSQSLDPLLELQVIEVALIRLOLI
 NMDEHKKVMGEVYGLSKDLQMLENLEMSLGIIRKKKQILIEDIOELTHKQSGSEV
 HOENFELFNFOAYGTSDPNAVNGDTISPYPDTISERSGSHIFQLPQNSDLRALY"

BASE COUNT 326 a 257 c 250 g 228 t
 ORIGIN

Query Match 13.8%; Score 176.8; DB 8; Length 1061;
 Best Local Similarity 61.6%; Pred. No. 2.1e-30;
 Matches 318; Conservative 0; Mismatches 192; Indels 6; Gaps 2;

QY 359 gatgggaggggaaagacgctgcatccgagatgatactccacgagcgagagtgag 418
 DB 133 GATGGGAGGGGGAAGATTGAGATTAAAGCGATGAGAACACCCACGCGAGGTGAC 192
 QY 419 cttctcaagcgccggaagcgatcttcaagaagcgagagctcgcatctcttcgca 478
 DB 193 CTTCTCAAGCGCGCAACGCGCTCTCAACAGAGCGCTACAGAGCTCCGTCCTCGCA 252
 QY 479 tgcggaggtcgctgcatctctccagacacggcgccgctcagagatccta---g 535

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Db 253 CGCGAGGTCGCCCTTCATCGTCTTCTCCACCCGCGGCCCTCTACGAGTACTCCAACTC 312
OY 536 caccagcaltgaatcagttatagatcgtaagcagc---caaggaagagcagcagc 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 313 CACAGCCTGAAACGACATTTGAACGATACAGAAAGCTTGCACTGATACACCAACAC 372
OY 593 cgtcgcaatcccaactcgagctlaagtttggcaaaaggagcagcagccttgagaca 652
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 373 TGGGACTGTCTGTGAGCTATTTCTCAGTATTTATCAGCAGACAGCAACCAATTACGCA 432
OY 653 acaactgcacaacttgcagaanaattalcgagcttgcagggagatgatatcttctggt 712
    ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 433 GCAATATACCAACTTACAGAACACTTAACAGGACTTTGATGGGAGTCTCTGAGCACAAAT 492
OY 713 gaatgltcaagaactgcagctccctggagaatcaatttgaacaagccttgcgtgtgtc 772
    || | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 493 GAGCCTTAGAGACTGAACAGCTGAGAGGCGAGACTGGAAGAGGCATCAACAAATAATAG 552
OY 773 cgcagaagaagacatctcttgaatagatgcagattgaatcgaagcagcagttt 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 553 AACAAAAAGAACGAGCTGTGTCCGCTGAATGCAATGCAATGCAAGAAAAAGGAGCGGA 612
OY 833 attcaccagaagaataacagactgtacaataagat 868
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Db 613 GATGCATATATGATTAACATGTACTTGCGAAATPAAGAT 648
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Search completed: August 11, 2002, 08:37:19
Job time: 101/9 sec

1

2

3

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 09:36:03 ; Search time 68.94 Seconds

(without alignments)
602.245 Million cell updates/sec

Title: US-09-970-624-2

Sequence: 1216
1 MGRCKIVIRIDNSTSHQVY.....PQNNIEPTAPKIGLQILP 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP RODENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_VIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1216	100.0	240	09FVN1	Q9FVN1 zea mays (m
2	729.5	60.0	234	P92927	P92927 antirrhinum
3	638.5	52.5	234	049351	049351 arabidopsis
4	636.5	52.3	234	09S138	09S138 arabidopsis
5	605	49.8	240	004061	004061 medicago sa
6	597.5	49.1	217	09FPP0	09FPP0 arabidopsis
7	589	48.4	239	09M2M4	09M2M4 arabidopsis
8	544	44.7	218	094ET1	094ET1 ipomoea bat
9	544	36.6	248	041352	041352 silene lat
10	435	35.8	261	040765	040765 picea abies
11	433.5	35.6	241	065112	065112 populus tri
12	431.5	35.5	241	065111	065111 populus tri
13	428.5	35.2	222	040766	040766 picea abies
14	427	35.1	225	09SBR3	09SBR3 cucumis sat
15	426.5	35.1	284	082732	082732 arabidopsis
16	425.5	35.0	222	09ZTV6	09ZTV6 pinus resin

17	425.5	35.0	225	10	043616	043616 petunia hyb
18	425	35.0	261	10	004406	004406 pinus radia
19	424.5	34.9	222	10	09S7I9	09S7I9 picea maria
20	424.5	34.9	222	10	09ZRC6	09ZRC6 picea maria
21	424.5	34.9	222	10	09ZTW4	09ZTW4 pinus radia
22	423.5	34.8	228	10	040882	040882 petunia hyb
23	423	34.8	246	10	09ZS29	09ZS29 gerbera hyb
24	422.5	34.7	249	10	09SMB3	09SMB3 oryza sativ
25	422	34.7	252	10	09STO6	09STO6 gnetum parv
26	422	34.7	253	10	09XG38	09XG38 gnetum gnem
27	420	34.5	237	10	09SBR1	09SBR1 cucumis sat
28	420	34.5	262	10	064958	064958 cucumis sat
29	419.5	34.5	228	10	09ZEP9	09ZEP9 hyacinthus
30	419.5	34.5	249	10	09SEV1	09SEV1 oryza sativ
31	416.5	34.3	254	10	09XG36	09XG36 cucumis sat
32	416	34.2	229	10	064959	064959 gnetum gnem
33	415.5	34.2	246	10	09XPM8	09XPM8 antirrhinum
34	415.5	34.2	264	10	09ZS30	09ZS30 gerbera hyb
35	414.5	34.1	221	10	09LKO1	09LKO1 cucumis sat
36	414.5	34.1	284	10	09FEB9	09FEB9 physcomitre
37	414	34.0	258	10	09S3H3	09S3H3 arabidopsis
38	414	34.0	270	10	09SPN2	09SPN2 oryza sativ
39	413	34.0	247	10	09XGK4	09XGK4 gnetum gnem
40	412	33.9	244	10	09XHM3	09XHM3 liquidambar
41	412	33.9	283	10	09FE71	09FE71 physcomitre
42	410	33.7	249	10	09MBE2	09MBE2 rosa rugosa
43	409	33.6	244	10	082128	082128 triticum ae
44	408	33.6	242	10	09ZTV9	09ZTV9 corlyus ave
45	407	33.5	254	10	09SBR2	09SBR2 cucumis sat

ALIGNMENTS

RESULT	ID	Q9FVN1	PRELIMINARY:	PRT:	240 AA.
AC	Q9FVN1	01-MAR-2001 (TREMBLREL. 16, Created)			
DT	01-MAR-2001 (TREMBLREL. 16, Last sequence update)				
DE	01-DEC-2001 (TREMBLREL. 19, Last annotation update)				
DI	MADS BOX PROTEIN 2.				
GN	MADS2.				
OS	Zea mays (Maize).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;				
OC	Panicoideae; Andropogoneae; Zea.				
OX	NCBI_TaxID=4577;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Al88;				
RA	Heuer S., Loez H., Dresselhaus T.;				
RT	"The MADS box gene ZmMADS2 is specifically expressed in maize pollen				
RT	und during maize pollen tube growth."				
RL	Sex. Plant Reprod. 13:21-27(2000).				
DR	EMBL; AF112149; AAG0919.1; -				
DR	HSSP; P11746; 1MN.				
DR	InterPro; IPR002487; K-box.				
DR	InterPro; IPR002100; MADS-box.				
DR	Pfam; PF01486; K-box; 1.				
DR	Pfam; PF00319; SRF-TE; 1.				
DR	PRINTS; PR00404; MADSOMAIN.				
DR	SMART; SM00432; MADS; 1.				
DR	PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.				
DR	PROSITE; PS00066; MADS_BOX_2; 1.				
SQ	SEQUENCE 240 AA: 27415 MW: 59941655CDDED984 CRC64:				

Query Match 100.0%; Score 1216; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.6e-76;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 60
QY 61 SSKSVIDRYGKAKEEQVAVANPNSSEKFWQREASLSRQOLHNLQENYQOLTGDDLSGLNY 120
Db 61 SSKSVIDRYGKAKEEQVAVANPNSSEKFWQREASLSRQOLHNLQENYQOLTGDDLSGLNY 120
QY 121 KELOSLLENQLETSLSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIRQENDEL 180
Db 121 KELOSLLENQLETSLSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIRQENDEL 180
QY 181 HKKITETEGSGVNSPPTPEFNAVEETRDVVOLELSTLPQONNIEPSTAKIGLQILIP 240
Db 181 HKKITETEGSGVNSPPTPEFNAVEETRDVVOLELSTLPQONNIEPSTAKIGLQILIP 240

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RESULT 2
P92927 PRELIMINARY; PRT; 234 AA.
AC P92927;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DEF125 PROTEIN.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97336298; PubMed=9193074;
RA Zachgo S., Seidler H., Schwartz-Sommer Z.;
RT Pollen-specific expression of DEF125, a MADS-box transcription
RT factor in Antirrhinum with unusual features."
RL Plant J. 11:1043-1050(1997).
DR EMBL: Y10750; CAAT71739.1; -.
DR HSSP: P11746; 1NMW.
DR TRANSFAC: T03080; -.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR InterPro: IPR001854; Ribosomal_L29.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 234 AA; 26882 MW; D69B216DD4FBE93 CRC64;

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Query Match 60.0%; Score 729.5; DB 10; Length 234;
Best Local Similarity 63.2%; Pred. No. 5.3e-43;
Matches 146; Conservative 32; Mismatches 52; Indels 1; Gaps 1;
QY 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 60
Db 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 60
QY 61 SSKSVIDRYGKAKEEQVAVANPNSSEKFWQREASLSRQOLHNLQENYQOLTGDDLSGLNY 120
Db 61 SSKSVIDRYGKAKEEQVAVANPNSSEKFWQREASLSRQOLHNLQENYQOLTGDDLSGLNY 120
QY 121 KELOSLLENQLETSLSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIRQENDEL 180
Db 121 KELOSLLENQLETSLSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIRQENDEL 180
QY 181 HKKITETEGSGVNSPPTPEFNAVEETRDVVOLELSTLPQONNIEPSTAKIGLQILIP 240
Db 181 CKRAYGRDVSANGTALVAFGALRGREPEPIQLHLSQ-PEPENIETSR 230

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RESULT 3

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049351
ID 049351 PRELIMINARY; PRT; 234 AA.
AC 049351;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANR1, MADS-BOX PROTEIN.
GN ANR1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=LANDSBERG ERCTA (LER);
RX MEDLINE=98092528; PubMed=9430595;
RA Zhang H., Forde B.G.;
RT "An Arabidopsis MADS box gene that controls nutrient-induced changes
RT in root architecture."
RL Science 279:407-409(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: Z97057; CAB09793.1; -.
DR HSSP: P11831; 1SR5.
DR TRANSFAC: T03034; -.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 234 AA; 26805 MW; 721A03A018E25527 CRC64;

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Query Match 52.5%; Score 638.5; DB 10; Length 234;
Best Local Similarity 54.9%; Pred. No. 1e-36;
Matches 135; Conservative 47; Mismatches 43; Indels 21; Gaps 5;
QY 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 59
Db 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 59
QY 60 TSKSVIDRYGKAKEEQVAVANPNSSEKFWQREASLSRQOLHNLQENYQOLTGDDLSGLNY 119
Db 61 SSKSVIDRYGKAKEEQVAVANPNSSEKFWQREASLSRQOLHNLQENYQOLTGDDLSGLNY 120
QY 120 VELOSLLENQLETSLSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIRQENDEL 179
Db 121 ANDLOLEQLETSLSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIRQENDEL 180
QY 180 LKKITETEGSGVNSPPTPEFNAVEETRDVVOLELSTLPQONNIEPSTAP 232
Db 181 LKKITETEGSGVNSPPTPEFNAVEETRDVVOLELSTLPQONNIEPSTAP 232
QY 233 KLGLOL 238
Db 233 KLGLOL 238
QY 228 RIGLOL 233
Db 228 RIGLOL 233

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RESULT 4
09S138 PRELIMINARY; PRT; 234 AA.
ID 09S138;
AC 09S138;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE MADS-BOX PROTEIN ANR1.
GN AT2G14210.
OS Arabidopsis thaliana (Mouse-ear cress).

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euposids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; Pubmed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL; AC007210; AAD25638.1; -;
 DR HSSP; P11831; 1SR5.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 KW SEQUENCE 234 AA; 26803 MW; 720F16BC1F72DE27 CRC64;
 SQ

Query Match 52.3%; Score 636.5; DB 10; Length 234;
 Best Local Similarity 54.9%; Pred. No. 1.4e-36;
 Matches 135; Conservative 46; Mismatches 44; Indels 21; Gaps 5;

QY 1 MGRGIVIRIDNSTSRQVTFESKRRNGIFKKAKELALICDPAVGVIFFSGRLYEY-SS 59
 DB 1 MGRGIVIRIDNSTSRQVTFESKRRSGLIKAKELSLICDPAVGVIFFSGRLYDIASN 60
 QY 60 TMSKVIDRYGKAKEEQVAVNPNSLKFQREASLSRQOLHNLOENYROLTGDDLSGLN 119
 DB 61 SSMKTIIEYNNKVEQHQHLLHNAEIKFQWQEVASLQOQLOYLQDCHRKLVGELSGMN 120
 QY 120 VKELOSLENOLETSLRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLQENDE 179
 DB 121 ANDLLENOLEDTLSLKGVALKXKQDLQMTNRELNRRKQGLQIQEKNELNIDVIMKEINK 180
 QY 180 LHKKTY----ETEGSGVAVRESPTFNFVAVETRVVPVQLESTL---PQONNIPESTAP 232
 DB 181 LQKKVAGRTNAIEGNSVDPISNGTTTYA-----PQQLQLQLQAPAPREKSI----- 227
 QY 233 KLGLOL 238
 DB 228 RLGLOL 233
 RESULT 5
 ID 004061 PRELIMINARY; PRT; 240 AA.
 AC 004061
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MADS-BOX PROTEIN (FRAGMENT).
 OS Medicago sativa (Alfalfa).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euposids II; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Dunn K., Heard J.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U91964; AAB51377.1; -;
 DR HSSP; P11746; 1MM.
 DR TRANSFAC; T03108; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR NON TER 1
 FT SEQUENCE 240 AA; 27138 MW; 3E38E21392594D14 CRC64;
 SQ

Query Match 49.8%; Score 605; DB 10; Length 240;
 Best Local Similarity 53.6%; Pred. No. 2.1e-34;
 Matches 128; Conservative 32; Mismatches 41; Indels 38; Gaps 4;

QY 3 RGVIVIRIDNSTSRQVTFESKRRNGIFKKAKELALICDPAVGVIFFSGRLYEYSSSM 62
 DB 1 RGVIVIRIDNSTSRQVTFESKRRNGLIKAKELALICDPAVGVIFFSGRLYDIPSTSL 60
 QY 63 KSVIDRYGKAKEEQVAVNPNSLKFQREASLSRQOLHNLOENYROLTGDDLSGLNKE 122
 DB 61 RSVIGRYNNKSEEHNOGSTASEIKFCQREAAVLRQOLHNLQSHHQIMGEELSGLTVE 120
 QY 123 LOSLENOLETSLRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLROENDELK 182
 DB 121 LQGLENOLETSLSRGVRAKKDQLEFDETOELNRRKGDIIHOENVELY-----R 166
 QY 183 KIVTEGSGVNR-----ESPFPNFVAVETRVVPV---OLELSTL 220
 DB 167 KVGITKDKNGINRVLSLTNGVIGDSDNRICEPAAO---PATERRTTALMHSLEISVL 222
 RESULT 6
 ID 09PPO PRELIMINARY; PRT; 217 AA.
 AC 09PPO;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MADS-BOX PROTEIN AGL16 (FRAGMENT).
 CN AGL16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF, STEM, ROOT;
 RX MEDLINE=20566573; Pubmed=1115127;
 RA Alvarez-Buylla E.R., Liljegren S.J., Pelaz S., Gold S.E., Burgeff C.,
 RA Ditta G.S., Vergara-Silva F., Yanofsky M.F.;
 RT "MADS-box gene evolution beyond flowers: expression in pollen,
 endosperm, guard cells, roots and trichomes.";
 RL Plant J. 24:457-466(2000).
 DR EMBL; AF312662; AAG37899.1; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.

FT NON_TER 1 1
 SQ SEQUENCE 217 AA; 24853 MW; 8C0E7816396D26BB CRC64;

Query Match 49.1%; Score 597.5; DB 10; Length 217;
 Best Local Similarity 57.8%; Pred. No. 6.1e-34;
 Matches 122; Conservative 38; Mismatches 50; Indels 1; Gaps 1;

QY 24 RRRGIFKKAKELALICDAEVLFFSTGRLEYESTSMKSVIDRKAKKEQOVANPN 83
 DB 1 RRRGIFKKAKELALICDAEVLFFSTGRLEYESTSMKSVIDRKAKKEQOVANPN 60
 QY 84 SELKFWQREASLRQOLHNLQENYRQLTGDDSLGNYKELQSLQENQLETSLRGVRACKDH 143
 DB 61 SEIOFWQREASLRQOLHNLQENYRQLTGDDSLGNYKELQSLQENQLETSLRGVRACKDH 120
 QY 144 LLIDEIHDNLNKKASLFFHOENTDLYNKINLROENDELHKKIYETEGSGVNSPPTPFNF 203
 DB 121 MLIEIOLVNLNKKASLFFHOENTDLYNKINLROENDELHKKIYETEGSGVNSPPTPFNF 180
 QY 204 AVETRDVYQLESLTLPOQNNIEPSTAPKL 234
 DB 181 DMRTSNEHVHLQSLQ-PQHDHETHSKAIQL 210

RESULT 7
 Q9M2M4 PRELIMINARY; PRT; 239 AA.

AC Q9M2M4;
 DT 01-OCT-2000 (TREMREL. 15, Created)
 DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE MADS-BOX TRANSCRIPTON FACTOR-LIKE PROTEIN.
 GN F2809.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benes V., Rechmann S., Borkova D., Ansojge W., Mewes H.W., Lemcke K.,
 Mayer K.F.X., Queller F., Salanoubat M.,
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL137080; CAB68129.1; -
 DR HSSP; P11746; 1MNM.
 DR InterPro; IPR002487; K-box.
 DR InterPro; IPR002100; MADS-box.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS_1.
 DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 SQ SEQUENCE 239 AA; 27233 MW; CE420AC4F98D45DB CRC64;

Query Match 48.4%; Score 589; DB 10; Length 239;
 Best Local Similarity 53.3%; Pred. No. 2.6e-33;
 Matches 130; Conservative 39; Mismatches 53; Indels 22; Gaps 4;

QY 1 MGRGKIVIRIDNSTSRQVTFKRRNGIFKKAKELALICDAEVLFFSTGRLEYEST 60
 DB 1 MGRGKIVIRIDNSTSRQVTFKRRNGIFKKAKELALICDAEVLFFSTGRLEYEST 60
 QY 61 SKMSVDRGKAKKEQOVANPNSELKFWQREASLRQOLHNLQ-ENY-----ROL 110
 DB 61 SKMSVDRGKAKKEQOVANPNSELKFWQREASLRQOLHNLQ-ENY-----ROL 110

QY 111 TGGDLSGLNWEKQSLQENQLETSLRGVRACKDHLLIDEIHDNLNKKASLFFHOENTDLYNKI 170
 DB 110 MGEISGLSVLEALQNLQENQLETSLRGVRACKDHLLIDEIHDNLNKKASLFFHOENTDLYNKI 169
 QY 171 NLIROENDELHKKIYETEGSGVNSPPTPFNFVAVETRDVYQLESLTLPOQNNIEPST 230
 DB 170 NLIROENDELHKKIYETEGSGVNSPPTPFNFVAVETRDVYQLESLTLPOQNNIEPST 228
 QY 231 AKRL 234
 DB 229 AIQL 232

RESULT 8
 Q94ET1 PRELIMINARY; PRT; 218 AA.

AC Q94ET1;
 DT 01-DEC-2001 (TREMREL. 19, Created)
 DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE MADS-BOX PROTEIN.
 GN MADS1.
 OS Ipomoea batatas (Sweet potato) (Batale).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxID=4120;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haung Y.-S., Yeh K.-W.,
 RT "Cloning and characterization of a full-length cDNA encoding a MADS-
 box protein from sweet potato."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF396746; AAK83920.1; -
 SQ SEQUENCE 218 AA; 25222 MW; 788D47FEB8D02DC8 CRC64;

Query Match 44.7%; Score 544; DB 10; Length 218;
 Best Local Similarity 50.0%; Pred. No. 3e-30;
 Matches 112; Conservative 46; Mismatches 48; Indels 18; Gaps 5;

QY 1 MGRGKIVIRIDNSTSRQVTFKRRNGIFKKAKELALICDAEVLFFSTGRLEYEST 60
 DB 1 MGRGKIVIRIDNSTSRQVTFKRRNGIFKKAKELALICDAEVLFFSTGRLEYEST 60
 QY 61 SKMSVDRGKAKKEQOVANPNSELKFWQREASLRQOLHNLQ-ENY-----ROL 119
 DB 61 SKMSVDRGKAKKEQOVANPNSELKFWQREASLRQOLHNLQ-ENY-----ROL 119
 QY 120 VKEIQLSENOLETSLRGVRACKDHLLIDEIHDNLNKKASLFFHOENTDLYNKINLROEND 178
 DB 120 VKDIQLSENOLETSLRGVRACKDHLLIDEIHDNLNKKASLFFHOENTDLYNKINLROEND 171
 QY 179 ELHKIYETEGSGVNSPPTPFNFVAVETRDVYQLESLTLPO 222
 DB 172 ---QAVGTSDPNNAVNGPTISPYDFTISESOGHIFQ---LPO 208

RESULT 9
 Q41352 PRELIMINARY; PRT; 248 AA.

AC Q41352;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE SIM1 PROTEIN.
 GN SIM1.
 OS Silene latifolia.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=37657;
 RN [1]


```

Db      16 LDRGKEIRIENITNTNRQVTFCKRRNGILKAKYELSVLDCDEVALIVFSSRRRELEYSSNN 75
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 SMKSVYDRGKA---KEEQVAVANNSELKFWOREASLROOLHNLJOENVRLTGDDLSG 11
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      76 SVKSTLIERKKKACADSSNNNGSSVANAQ--FYQDAKLRSQIGMLQNSNRMLSESLA 13
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      118 LNKLELSTLENOLFSLRGVRAKKDHLIDETHIDLNKASLFHOENDTLYNKINIR--- 17
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      134 LSVKELKSLLEIKLEKIGIRSKKNELLFAETIEMQKR-----EIDLHNNQLLRAKI 18
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      175 QENDELHKIYETEGSPVNR--SPFPFN 202
      11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      187 AENE--RRQHNMIMGVNFEMOSQFPF 214
      11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
065111
AC      065111: PRELIMINARY; PRT: 241 AA.
DT      01-AUG-1998 (TREMBLrel. 07, Created)
DT      01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      AGAMOUS HOMOLOG.
GN      PTAG1.
OS      Populus trichocarpa (Western balsam poplar).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids I; Malpighiales; Salicaceae; Populus.
OX      NCBI_TaxID=3694;
      (1)
RN      SEQUENCE FROM N.A.
RP      Brunner A.M., Rottmann W.H., Sheppard L.A., Strauss S.H.;
RT      "Two Populus trichocarpa genes homologous to AGAMOUS.";
RL      Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC      -I- SIMILARITY: TO THE EMBL/GenBank/DBJ SIMILARITY.
CC      -I- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR      EMBL; AF052570; AAC06237.1; -.
DR      HSSP; P11746; IMNM.
DR      InterPro: IPR002487; K-box.
DR      InterPro: IPR002100; MADS-box.
DR      Pfam; PF01486; K-box; 1.
DR      Pfam; PF00319; SRF-TF; 1.
DR      PRINTS; PR00404; MADSDOMAIN.
DR      SMART; SM00432; MADS; 1.
DR      PROSITE; PS00350; MADS_BOX_1; 1.
DR      PROSITE; PS50066; MADS_BOX_2; 1.
KW      DNA-binding; Nuclear protein; Transcription regulation.
      SEQUENCE 241 AA; 27559 MW; 4C2BD11F29599CF CRC64;
      SO

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[illegible]

RESULT	ID	PRELIMINARY;	PRT;	222 AA.
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AC	Q40766;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	DAL2 PROTEIN.			
GN	DAL2.			
OS	Abies abies (Norway spruce) (Picea excelsa).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta, Coniferopsida; Coniferales; Pinaceae; Picea.			
CN	NCBI_taxid=3329;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=FEMALE CONE.			
RA	MEDLINE=95170009; PubMed=7865797;			
RT	Tandere K., Albert V.A., Sundas A., Engstrom P.,			
RT	"Conifer homologues to genes that control floral development in			
RT	angiosperms.";			
RL	Plant Mol. Biol. 27:69-78(1995).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.			
DR	EMBL; X79280; CAA55867.1; -.			
DR	HSSP; P11746; IMNM.			
DR	TRANSFAC; T03076; -.			
DR	InterPro; IPR002487; K-box.			
DR	InterPro; IPR002100; MADS-box.			
DR	Pfam; PF01486; K-box_1.			
DR	Pfam; PF00319; SRP-TE; 1.			
DR	PRINTS; PR00404; MADSDOMAIN.			
DR	SMART; SM00432; MADS; 1.			
DR	PROSITE; PS00350; MADS_BOX_1; 1.			
DR	PROSITE; PS50066; MADS_BOX_2; 1.			
KW	DNA-binding; Nuclear protein; Transcription regulation.			
SO	SEQUENCE 222 AA; 25638 MW; 53699DB6288F77D9 CRC64;			

[illegible]

7
:
:

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 08:37:25 ; Search time 61.65 Seconds
(without alignments)
432.404 Million cell updates/sec

Title: US-09-970-624-2
Perfect score: 1216
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1216	100.0	240	22	Maize zmmads2 seq
2	1216	100.0	240	22	Maize zmmads2 prot
3	666	54.8	228	21	Arabidopsis thalia
4	643.5	52.9	227	21	Arabidopsis thalia
5	636.5	52.3	234	21	Arabidopsis thalia
6	633.5	52.1	238	21	Arabidopsis thalia
7	433.5	35.6	238	21	Poplar PTAG-2 flori
8	433.5	35.6	238	22	Poplar PTAG-2 flori
9	431.5	35.5	241	21	Amino acid sequenc
10	431.5	35.5	241	21	Poplar PTAG-1 flori
11	431	35.4	185	21	Amino acid sequenc
					Eucalyptus grandis

12	431	35.4	229	17	AA999637	Eucalyptus AGE-2 p
13	426.5	35.1	300	21	AA952721	Arabidopsis thalia
14	425	35.0	261	19	AAW48623	Pinus radiata cone
15	424.5	34.9	222	21	AAW26795	Plant reproductive
16	420	34.5	221	21	AAW44804	Petunia hybrida ne
17	420	34.5	221	21	AAW58648	Petunia nectary-sp
18	419.5	34.5	230	21	AAW16690	Arabidopsis thalia
19	419.5	34.5	230	21	AAW40213	Arabidopsis thalia
20	419.5	34.5	277	21	AAW16689	Arabidopsis thalia
21	419.5	34.5	277	21	AAW40212	Arabidopsis thalia
22	417	34.3	246	20	AAW81000	Arabidopsis AGU5 p
23	414	34.0	251	21	AAW34121	Zea mays protein f
24	414	34.0	258	21	AAW32583	Arabidopsis thalia
25	414	34.0	307	21	AAW34120	Zea mays protein f
26	412.5	33.9	262	21	AAW69920	MADS box protein.
27	407	33.5	167	21	AAW31143	Arabidopsis thalia
28	406	33.4	268	21	AAW43856	Zea mays protein f
29	405	33.3	248	20	AAW80999	Arabidopsis AGU1 p
30	405	33.3	248	21	AAW09411	Arabidopsis thalia
31	402.5	33.1	242	19	AAW48622	Pinus radiata cone
32	402	33.1	257	21	AAW33135	Zea mays protein f
33	402	33.1	260	21	AAW33134	Zea mays protein f
34	402	33.1	283	21	AAW33133	Zea mays protein f
35	401	33.0	248	20	AAW84050	Rice OSMADS8 prote
36	401	33.0	251	17	AAW99633	Eucalyptus AGE-1 p
37	401	33.0	257	17	AAW99631	OSMADS1 protein.
38	398	32.7	181	21	AAW33310	Pinus radiata tran
39	396.5	32.6	161	21	AAW33229	Eucalyptus grandis
40	395.5	32.5	240	21	AAW96767	Z. mays MADS-box p
41	393	32.3	253	19	AAW69329	Brassica oleracea
42	393	32.3	253	19	AAW43110	APETAL1 gene prod
43	393	32.3	253	19	AAW39132	Brassica floral me
44	393	32.3	253	19	AAW43327	Brassica floral me
45	393	32.3	253	21	AAW19242	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAB72888
ID AAB72888 standard; Protein; 240 AA.
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AC AAB72888;
XX
DT 11-MAY-2001 (first entry)
XX
DE Maize zmmads2 SEQ ID NO: 2.
XX
KW Male sterile plant; maize; hybrid breeding; pollen tube; zmmads2;
KW grain; cereal; corn.
XX
OS Zea mays.
XX
PN WO200112798-A2.
XX
PD 22-FEB-2001.
XX
PF 16-AUG-2000; 2000WO-EP08001.
XX
PR 18-AUG-1999; 99EP-0116267.
XX
(SUED-) SUEDEWESTDEUTSCHE SAATZUCHT.
XX
PI Loerz H, Dresselhaus T, Schreiber D, Heuer S;
XX
DR WPI; 2001-211213/21.
XX
N-PSDB; AAF76445.
XX
Novel nucleic acid molecule, zmmads2 derived from pollen of Zea mays
PT useful for cloning and expressing a pollen specific sequence in a plant
PT and for producing male sterile plants -
XX

PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132865.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
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PR 29-OCT-1999; 9905-0162142.

Query Match 54.8%; Score 666; DB 21; Length 228;

Best Local Similarity 59.0%; Pred. No. 2,36-52; Matches 138; Conservative 36; Mismatches 50; Indels 10; Gaps 3;

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OY 61 SMKSVADRGRGKAKEEOVVANPNSELEKQWRPAASIRQQLHNDQENYRQLTSDGLNV 120
DB 61 smksvadrgrgkakeeoovvanpnselekwrpasirqqllhndqenyrqltsdglnv 120
OY 121 KETQSLQENLETSLRGVRAKDHLLIDEIHDINRKASLFEHONTLOLYNKINIRQENDEL 180
DB 121 ketqslqenleTSLRGVRAKDHLLIDEIHDINRKASLFEHONTLOLYNKINIRQENDEL 180
OY 181 HKKIYTESPSSVNRSPFPNFVAVERD-VPVQLESLTPQNNIEPSTAPK 233
DB 181 hkkitytespssvnrspfpnfvaVERD-VPVQLESLTPQNNIEPSTAPK 233
DB 181 ykKaymanngfthre----vavadeshtqirqlgs--qphsdydipr 225

RESULT 4

AAAG32045 standard; Protein; 227 AA.

AAAG32045;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 38587.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

XX EPI033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 9905-0121825.

XX PR 05-MAR-1999; 9905-0123180.

XX PR 09-MAR-1999; 9905-0123548.

XX PR 23-MAR-1999; 9905-0125788.

XX PR 25-MAR-1999; 9905-0126264.

XX PR 29-MAR-1999; 9905-0126785.

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PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

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Query Match 52.9%; Score 643.5; DB 21; Length 227;
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Db 1 mrgkiviridkstsrqvtfskrmrqgikkkakelalldaevalifsncklydfass 60
QY 61 SMKSIDRYGKAKEEQOVVANPNSELKFWOREASLRQOLNHLQBNYRQLTGDDLSGLNY 120
Db 61 svkstlerfntakmeeqelmpasevkkfwgreaetlrgelhslgennyqltgvvelnglsv 120
QY 121 KELOSLENOLETSLKGVAKKDHLLIDETIDHNKRKASLPHQONTLQYKINILROENDEL 180
Db 121 kelglsesqlslmrlgirkreqlltneikeltlrnlyvhenlelsrkvyqihgenvei 180
QY 181 HKRIYETEGSGVNRSEPRPFNFVETRDVPVQLESLTPQONNIETPST 230
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RESULT 5
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ID AAC30615 standard; Protein; 234 AA.
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AC AAG30615;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SPQ ID NO: 36633.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 990S-0121825.

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PR 05-OCT-1999; 99US-0157753.
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Query Match 52.3%; Score 636.5; DB 21; Length 234;
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QY 60 TSMKGVIRRYGKAKKEQOVVAPNSELKFWOREASLRQOLHNLENTYROTGLDLSGLN 119
DB 61 SEMKILIEYRNVKEEGQIHLHASELKFQREVSLQDQIYIQCENRKLVEELSgmn 120
QY 120 VKEILOSLENOLETSLRGVRAKKDHLLIDEIHLNKKASLPHOENTDLYXNKINLRQENDE 179
DB 121 andlqnedqlytsikyryllkkdqimneirelnkqgiqlqenhelqivdimrkenik 180
QY 180 LHKRTY---ETEGPSGVNRESPTPFNFVAVETRPVQLELSTL---PQONNTERSTAP 232
DB 181 lqkvhygrtnalegnsvdpisnglttya-----ppqlqilqipapreksi----- 227
QY 233 KGLQL 238
DB 228 rlgql 233
RESULT 6
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ID AAG50753 standard; Protein: 238 AA.
XX AAG50753;
XX 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 64351.
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 02-JUL-1999; 99US-0142154.
 PR 06-JUL-1999; 99US-0142055.
 PR 08-JUL-1999; 99US-0142390.
 PR 09-JUL-1999; 99US-0142803.
 PR 12-JUL-1999; 99US-0142920.
 PR 13-JUL-1999; 99US-0142977.
 PR 14-JUL-1999; 99US-0143542.
 PR 15-JUL-1999; 99US-0143624.
 PR 16-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0145086.
 PR 22-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 10-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148664.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154479.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
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 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 52.1%; Score 633.5; DB 21; Length 238;
 Best Local Similarity 54.0%; Pred. No. 2.1e-49;
 Matches 135; Conservative 45; Mismatches 45; Indels 25; Gaps 5;

QY 1 MGRGKIVIRINDNSTROVTEPSKRRNGJFKKAKELATTCDAEYGVITSPSGRLYEVSST 60
 Db 1 mrggkivirindnstrovtetsqytlstksrtsgllkkakelellcdaevgyvlftstgklydyasn 60
 QY 61 -----SMKSVIDRYGKAKEEQVAVNPNSSELKFMOREAASIROQLAHNTQENVROLTGDDL 115
 Db 61 srlpscmktlierynrvnveeqqllnhaselkfwgrevaslqqqyqlgechrklvgeel 120
 QY 116 SGLNKELOSLBNQLETSIRGVRAKKDHLIDELHDLNRKASLFEQENTDLYNKNILIRQ 175
 Db 121 sygnndlnqledqlvtstlkyvrlkkdqlmtnelrlnrkqylqkhenheignlvdmrk 180
 QY 176 ENDELHKKRY----ETEGPSGVNRESPTFPNRAVETRDVVOLESLT---POONNTEP 228
 Db 181 enlklyqkvhgrtnaiegnssvdpisngtltva-----ppqlqlqlqapapreksl-- 231
 QY 229 STAPKLGLOL 238
 Db 232 ----rlqlql 237
 RESULT 7
 AAY58657
 ID AAY58657 standard; Protein: 238 AA.
 XX
 AC AAY58657;

[illegible][illegible]

Db 76 svksltlerykkacadsnngsvseanaq--fygqaeklirsgnlgnsnrmlgesisa 133
 QY 118 LNVKELOSLENQLETSLRGVRAKKDHLIDELHDLNRKASLFHQENTDLYNKINILIR-- 174
 Db 134 lsvkelksleirlekysirskkneillfaeleymqkr-----edlhnngqlliraki 186
 QY 175 QENDELHKKIYETEGSPGVNRE--SPTEPN 202
 Db 187 aene--rkrqhmhmpgyvfeimsgpfd 214

RESULT 9
 AAY58656
 ID AAY58656 standard; Protein; 241 AA.
 AC AAY58656;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Poplar PRAG-1 floral homeotic gene-encoded protein.
 XX
 KW Poplar; PRAG-1; floral homeotic gene; transgenic plant; sterility;
 XX fertility.
 OS Populus balsamifera subsp. trichocarpa.
 XX
 FH Key Location/Qualifiers
 FT Domain 17..33
 FT /note= "MADS domain"
 FT 106..172
 FT /note= "K domain"
 XX
 PN CA2227940-A1.
 XX
 PD 06-OCT-1999.
 XX
 PF 07-APR-1998; 98CA-2227940.
 XX
 PR 06-APR-1998; 98US-0080851.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
 XX
 DR WPI: 2000-106662/10.
 DR N-PSDB; AAZ57946, AAZ57947.
 XX
 PT Nucleic acid from Populus trichocarpa genes, useful for producing
 PT transgenic plants, particularly trees, with modified fertility
 PT characteristics such as sterility -
 XX
 PS Claim 31; Page 67-68; 92pp; English.
 XX
 CC The present sequence is that of the novel PRAG-1 protein of poplar
 CC (Populus balsamifera subsp. trichocarpa), as deduced from newly
 CC isolated gene and cDNA sequences (see AAZ57946-47). PRAG-1 is 1
 CC of 4 novel floral homeotic genes identified in this poplar species.
 CC It is a homologue of AGAMOUS and is expressed in floral tissues.
 CC PRAG-1 contains a MADS domain and a K-domain. The invention
 CC provides nucleic acid sequences of the 4 novel Populus genes, the
 CC corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid
 CC sequences (see AAY58454-57). It also provides methods of using the
 CC gene and cDNA sequences to produce genetically engineered Populus
 CC and other trees having modified fertility characteristics, including
 CC sterility. Genetic constructs useful in producing genetically
 CC engineered Populus and other trees include antisense versions of
 CC PRAG-1, dominant negative mutants, and constructs useful for sense
 CC suppression. Sterile trees allow increased wood yield and a
 CC reduction in the production of allergens such as pollen.
 CC
 XX Sequence 241 AA;

Query Match 35.5%; Score 431.5; DB 21; Length 241;
 Best Local Similarity 40.0%; Pred. No. 4,4e-31;
 Matches 100; Conservative 52; Mismatches 63; Indels 35; Gaps 7;

QY 1 MGRKIVIRRDNTSROVFEKRRNRIFFKKAKELALICDAEGLYTFSTGRLYSSST 60
 Db 16 lgrgkveikritentlmqvclckrsglllkayelsvdcdaevalivfsrgrlyesnd 75
 QY 61 SMKSVIDRYKAKEEQD--VVANPNSELKFWQREASLRQOLHNIQENRROLTGDLG 117
 Db 76 svksltlerykkacadsnngsvseanaq--fygqaeklirsgnlgnsnrmlgesals 133
 QY 118 LNVKELOSLENQLETSLRGVRAKKDHLIDELHDLNRKASLFHQENTDLYNKINILROEN 177
 Db 134 lsvkelksleirlekysirskkneillfaeleymqkr-----evdlhnngqlliraki 186
 QY 178 DELHKKIYETEGSPGVNRES--PTPEFNAAVETEDVPQLESLRPLQNNIEP-----S 229
 Db 187 seneik-----rsgmnlmpygadfeivsq-----pydsrnysgvnglqpsahys 231

QY 230 TAPRLGLOLI 239
 Db 232 hgdqmalqlv 241

RESULT 10
 AAB68437
 ID AAB68437 standard; Protein; 241 AA.
 XX
 AC AAB68437;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Amino acid sequence of the floral homeotic protein PRAG-1.
 XX
 KW Floral homeotic gene; PTD; PTLF; PRAG-1; floral tissue; LEAFY;
 KW LEY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 XX fertility; sterility.
 OS Populus balsamifera.
 XX
 FH Key Location/Qualifiers
 FT Domain 17..72
 FT /note= "MADS domain"
 FT 106..172
 FT /note= "K domain"
 XX
 PN CA2319853-A1.
 XX
 PD 01-APR-2001.
 XX
 PF 02-OCT-2000; 2000CA-2319853.
 XX
 PR 01-OCT-1999; 99US-0410464.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
 XX
 DR WPI: 2001-336098/36.
 DR N-PSDB; AAF85397, AAF85398, AAF85399.
 XX
 PT Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,
 PT particularly sterility -
 XX
 PS Claim 23; Page 56-57; 69pp; English.
 XX
 CC The present sequence represents a floral homeotic protein, designated
 CC PRAG-1, which is derived from Populus balsamifera subsp. trichocarpa.
 CC The specification also describes PTD, PTLF, and PRAG-2 proteins. The
 CC floral homeotic proteins are expressed in floral tissues. PTLF is a
 CC homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in

PR 21-APR-1999; 99US-0130449.

PR	23-APR-1999;	99US-01305011
PR	23-APR-1999;	99US-01308911
PR	28-APR-1999;	99US-0131449
PR	30-APR-1999;	99US-01320408
PR	30-APR-1999;	99US-0132407
PR	04-MAY-1999;	99US-01324484
PR	04-MAY-1999;	99US-01324485
PR	05-MAY-1999;	99US-01324486
PR	06-MAY-1999;	99US-01324486
PR	06-MAY-1999;	99US-01324487
PR	07-MAY-1999;	99US-01324653
PR	11-MAY-1999;	99US-0134256
PR	11-MAY-1999;	99US-0134218
PR	14-MAY-1999;	99US-01344219
PR	14-MAY-1999;	99US-01344221
PR	14-MAY-1999;	99US-01343370
PR	18-MAY-1999;	99US-0134768
PR	19-MAY-1999;	99US-01346941
PR	20-MAY-1999;	99US-01351124
PR	21-MAY-1999;	99US-01353553
PR	24-MAY-1999;	99US-0135629
PR	27-MAY-1999;	99US-01365922
PR	28-MAY-1999;	99US-0136782
PR	01-JUN-1999;	99US-0137222
PR	03-JUN-1999;	99US-01375528
PR	04-JUN-1999;	99US-0137502
PR	07-JUN-1999;	99US-0137724
PR	08-JUN-1999;	99US-0138094
PR	10-JUN-1999;	99US-01385470
PR	10-JUN-1999;	99US-0139119
PR	14-JUN-1999;	99US-01394552
PR	16-JUN-1999;	99US-01394553
PR	17-JUN-1999;	99US-01394954
PR	18-JUN-1999;	99US-01394554
PR	18-JUN-1999;	99US-01394610
PR	18-JUN-1999;	99US-01394611
PR	18-JUN-1999;	99US-01394656
PR	18-JUN-1999;	99US-0139457
PR	18-JUN-1999;	99US-01394558
PR	18-JUN-1999;	99US-0139459
PR	22-JUN-1999;	99US-0139617
PR	23-JUN-1999;	99US-0140353
PR	23-JUN-1999;	99US-0140354
PR	24-JUN-1999;	99US-0140695
PR	28-JUN-1999;	99US-0140823
PR	29-JUN-1999;	99US-01409911
PR	30-JUN-1999;	99US-0141287
PR	01-JUL-1999;	99US-0141842
PR	01-JUL-1999;	99US-0142154
PR	02-JUL-1999;	99US-0142055
PR	06-JUL-1999;	99US-0142390
PR	08-JUL-1999;	99US-0142803
PR	09-JUL-1999;	99US-0142920
PR	12-JUL-1999;	99US-0142977
PR	13-JUL-1999;	99US-0143542
PR	14-JUL-1999;	99US-0143624
PR	15-JUL-1999;	99US-0144005
PR	16-JUL-1999;	99US-0144086
PR	19-JUL-1999;	99US-0144325
PR	19-JUL-1999;	99US-0144331
PR	19-JUL-1999;	99US-0144332
PR	19-JUL-1999;	99US-0144333
PR	19-JUL-1999;	99US-0144334
PR	19-JUL-1999;	99US-0144335
PR	20-JUL-1999;	99US-0144352

XX (EBIN-) FB INVESTMENTS PTY LTD.
 PA Teasdale RD;
 PI
 XX WPI: 1998-230712/20.
 DR N-PSDB: AAV18014.
 XX
 PT Method of enhancing vegetative growth in plant - comprises use of
 PT expression cassette containing heterologous coding region expressing
 PT product which aborts development
 XX
 PS Disclosure: Fig 14; 96pp; English.
 XX

XX This is the amino acid sequence of the PRMADS3 protein of Pinus
 CC radiata, deduced from an isolated cDNA clone (see AAV18012).
 CC Expression of PRMADS3 is restricted to male and female cones. The
 CC PRMADS1, 2 and 3 proteins (see also AAW48622 and AAW48623) have been
 CC expressed in E. coli and characterised as DNA binding proteins.
 CC Their DNA binding consensus sequence is similar to that of the
 CC AGAMOUS protein. All 3 proteins bind a DNA sequence matching the
 CC consensus sequence of the CARG box. The invention relates to genes
 CC from reproductive tissues of Pinus radiata and Eucalyptus grandis
 CC and the use of the promoters (see AAV18013, AAV18015, AAV18017 and
 CC AAV18019-22) of such genes in expression cassettes used to modify a
 CC plant, especially a tree used in timber, pulp or fibre production,
 CC to increase vegetative growth and thus production of valuable
 CC material.
 XX
 SQ Sequence 261 AA;

Query Match 35.0%; Score 425; DB 19; Length 261;
 Best Local Similarity 40.8%; Pred. No. 1.9e-30;
 Matches 89; Conservative 44; Mismatches 61; Indels 24; Gaps 4;

QY 1 MGRKIVIRIRDNSTNQVTFSSRRNGIFKAKELALICDAEVLGVISSGRLYEVSST 60
 DB 1 mgrkviririridnstrnqvtfssrrngifkakealalicdaevlgvissgrlyefass 60
 QY 61 SMKSVIRRYGKAK-EEQOVVANPSELEKFWOREAASLRQOLHNIQENYRQULGDDLSGLN 119
 DB 61 smksvirrygkaks-eeqovvanpselekworeaslrqolhniqenyroqulgddls 119
 QY 120 VKELQSLLENQLETSLRGVRAKDKHLIDETIDLNKASLFFHOENTDLYNKINIREQENDE 179
 DB 120 vkelqslleenqletsrlgvrakdkhlidetidlnrkaslfhoentdlynkinireqen 179
 QY 180 LHKRIYEEGP---SGVRESPT-----PENFAVET 208
 DB 167 lqkriyeegegrdvtlgtgtsntntgtngpdsstnt 204

RESULT 15
 AAB26795
 ID AAB26795 standard; Protein; 222 AA.
 XX
 AC AAB26795;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Plant reproductive tissue promoter protein.
 XX
 KW Plant promoter; PRAG1; reproductive tissue; transgenic plant; cereal.
 XX
 OS Pinus radiata.
 XX
 PN WO200055172-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-NZ00031.
 XX

PR 17-MAR-1999; 99NZ-034715.
 XX
 PA (CART-) CARTER HOLT HARVEY LTD.
 PA (TASMAN-) TASMAN BIOTECHNOLOGY LTD.
 PA (UNMT) UNIV MICHIGAN TECHNOLOGICAL.
 XX
 PI Podila GK, Liu J, Karnosky DF;
 XX
 DR WPI: 2000-594442/56.
 DR N-PSDB: AAA99362, AAA99363, AAA99364.
 XX
 PT Novel plant reproductive tissue promoter, useful to produce plants
 PT which have a diminished reproductive capacity or which are sterile
 XX
 PS Disclosure: Figure 1; 51pp; English.
 XX

XX This invention relates to a novel plant promoter gene. The promoter is
 CC located in plant reproductive tissue, and the invention includes
 CC transgenic plants containing the promoter. The promoter can be used to
 CC produce plants which have a diminished reproductive capacity or which are
 CC sterile. The constructs can also be used to transform agronomically
 CC important plants in which modulation of reproductive capacity
 CC (particularly the timing and abundance of flowering) is desirable,
 CC e.g. cereals, rice, maize, wheat, barley, oats, rye, soybean and canola.
 CC The present sequence represents the protein encoded by the plant
 CC reproductive promoter (PRAG1) gene of the invention.
 XX

SQ Sequence 222 AA;
 Query Match 34.9%; Score 424.5; DB 21; Length 222;
 Best Local Similarity 50.3%; Pred. No. 1.7e-30;
 Matches 87; Conservative 35; Mismatches 46; Indels 5; Gaps 2;

QY 1 MGRKIVIRIRDNSTNQVTFSSRRNGIFKAKELALICDAEVLGVISSGRLYEVSST 60
 DB 1 mgrkviririridnstrnqvtfssrrngifkakealalicdaevlgvissgrlyefass 60
 QY 61 SMKSVIRRYGKAKKEEQ--VVANPSELEKFWOREAASLRQOLHNIQENYRQULGDDLSG 117
 DB 61 svkrlerykktcvcvnnhbgalsesnsq-ywqgeagkrlrqidllqnanhngdglta 118
 QY 118 LNVKELQSLLENQLETSLRGVRAKDKHLIDETIDLNKASLFFHOENTDLYNKI 170
 DB 118 lnkvelqslleenqletsrlgvrakdkhlidetidlnrkaslfhoentdlynkiskl 171

Search completed: August 11, 2002, 09:35:57
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 07:29:40 ; Search time 208.02 Seconds
(Without alignments)
10564.612 Million cell updates/sec

Title: US-09-970-624-1

Perfect score: 1280
Sequence: 1 gcacgagccgccttcgcgcca.....aaaaaaaaaaaaaaaaaaaa 1280

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1109.6	86.7	1268	22	MAF76058
2	1109.6	86.7	1268	22	MAF76058
3	463.4	36.2	5031	22	MAF76058
4	463.4	36.2	5031	22	MAF76058
5	265.6	20.8	687	21	AAAC42918
6	254.8	19.9	684	21	AAAC43252
7	245	19.1	310	22	AAF76056
8	245	19.1	310	22	AAF76056
9	236.2	18.5	705	21	AAAC42728

10	224.2	17.5	717	21	AAAC50308
11	188.4	14.7	706	21	AAAC55965
12	179.6	14.0	997	17	AAAT34432
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ALIGNMENTS

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DT 22-MAY-2001 (first entry)
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KW Maize MADS box gene; ZMMADS2; pollen-specific expression;
KW Pollen development; function; transgenic plant; male sterility;
XX hybrid seed production; ss.
XX
OS Zea mays.
XX
PN WO200112799-A2.
XX
PD 22-FEB-2001.
XX
PF 16-AUG-2000; 2000WO-EP08002.
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PR 18-AUG-1999; 99EP-0116268.
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XX Loerz H, Dresselhaus T, Schreiber D, Heuer S;
DR WPI: 2001-211214/21.
XX P-PSDB; AAF73333.
XX Novel nucleic acid molecule useful for cloning and expressing a pollen

XX Hybridisation assay: genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS *Arabidopsis thaliana*.
XX EPI03405-A2.
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DT 17-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP103405-A2.
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PD 06-SEP-2000.
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PR 21-OCT-1999;	99US-0160814.
PR 21-OCT-1999;	99US-0160815.
PR 22-OCT-1999;	99US-0160980.
PR 22-OCT-1999;	99US-0160981.
PR 22-OCT-1999;	99US-0160989.
PR 25-OCT-1999;	99US-0161404.
PR 25-OCT-1999;	99US-0161405.
PR 25-OCT-1999;	99US-0161406.
PR 26-OCT-1999;	99US-0161359.
PR 26-OCT-1999;	99US-0161360.
PR 26-OCT-1999;	99US-0161361.
PR 28-OCT-1999;	99US-0161920.

Db 421 aaaaaggaatcaactatgaacaatgaatcagagacttaatcgtaaggacaatcctc 480
Qy 837 caccagaanaatatacagacttgcataaagatcaacctgattcgcaagaanaatgatag 896
Db 481 caaaagagaatcacgagctacacaatatgtgatatataatgcgtaaggaaataataa 540
Qy 897 ttacataaaagatatatgatagacttaaggaaccaagtggagttaat 941
Db 541 tgcgaagaagaagttcatggaagaacaatgcgattgaagcaat 585

RESULT 10
AAC50308
ID AAC50308 standard; DNA; 717 bp.
XX AAC50308;
AC
XX
XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 64350.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW Metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP103405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131048.
PR 04-MAY-1999; 99US-0132407.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
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PR 18-JUN-1999; 99US-0139454.
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PR 22-JUN-1999; 99US-0139889.
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PR 24-JUN-1999; 99US-0140695.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
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PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.

Query Match	17.5%;	Score 224.2;	DB 21;	Length 717;
Best Local Similarity	62.6%;	Pred. No. 4.8e-50;		
Matches 374; Conservative	0;	Mismatches 208;	Indels 15;	Gaps 1

PI wood M, McGrath A, Shenk MA, Glenn M,
yy

Db 197 ctttgcgaacgcgaggtcgccctcatcgcttctccagtcgcgcctctatgat 256
 QY 531 tctagcaccagcatgaatcatgattatagatcggtacgcgcaagggcaagagcaagca 590
 Db 257 gccacagatagtgctcaaaagcaaccatcgagaggtacaaagaggtcttctcagattc 316
 QY 591 gtcgtcgcaaa--atcccaactcgaggttaagtttgcaagggagcgcaagcttg 647
 Db 317 agtagcgagatccgttctgaagctaatgttctgatttatacgaagaatccgcaagttg 376
 QY 648 agacacacactgcacaacttgcagaataatcatcgcgagttgacggagatgattctt 707
 Db 377 caacacacgattatcaatcatgcaagacataacagcaactggtggtgactcattgct 436
 QY 708 ggcgtgaatgtlcaagaactcagtcctcgtggaatcaattggaacacagctcggtg 767
 Db 437 gggatgatatgaagatatagaagactactgagcaaaaactagaanaagcaatcgctaa 496
 QY 768 gtcgcgcaaaagagaccatctcttgatagatgagattcagattgaaatcgaaagca 827
 Db 497 attcgcgcaaaagagatgagcttctatttgcgagattggtatatacgaagggaa 556
 QY 828 agttatttcccaagaataacacgacttgcacaataagatc 869
 Db 557 atgcacctacaacaacatacgaatgtctgcgagcggaagatc 598

RESULT 13

AAAF76067
ID AAF76067 standard; DNA; 251 BP.

AAAF76067;

22-MAY-2001 (first entry)

Maize MADS-box gene ZMMADS2 3' regulatory element, SEQ ID NO:11.

KW Maize MADS box gene: ZMMADS2; 3' regulatory element;
 KW pollen-specific expression; pollen development; function;
 KW transgenic plant; male sterility; hybrid seed production; ds.

OS Zea mays.

WO200112799-A2.

22-FEB-2001.

16-AUG-2000; 2000WO-EP08002.

18-AUG-1999; 99EP-0116268.

(SUED-) SUEDEWESTDEUTSCHE SAATZUCHT.

Loerz H, Dresselhaus T, Schreiber D, Heuer S;

WPI: 2001-211214/21.

Novel nucleic acid molecule useful for cloning and expressing a pollen
 specific sequence in a plant -
 Claim 1; Page 60; 66pp; English.

CC The invention relates to regulatory elements (AAAF76059-AAAF76067) from
 CC the maize MADS box gene ZMMADS2 (AAAF76068) which are capable of directing
 CC expression in a pollen-specific manner. The ZMMADS2 protein (AAAF73333)
 CC is expressed particularly in mature pollen after dehiscence, indicating
 CC that it has an essential role in pollen development and function, in
 CC particular in pollen tube growth. The invention also relates to vectors
 CC and host cells comprising the ZMMADS2 regulatory or genomic sequence, and
 CC their use in the generation of transgenic plants. The ZMMADS2 regulatory
 CC sequences are useful for cloning and expressing a pollen-specific or
 CC pollen-abundant gene in a plant, and may also be used to drive the

CC expression of a gene of interest in a pollen-specific or pollen-preferred
 CC manner. The ZMMADS2 regulatory sequences are useful for isolating related
 CC regulatory sequences of other plant species which confer pollen or group
 CC specificity to genes of interest operably linked to them. The regulatory
 CC sequences are useful in plant breeding, especially for the production of
 CC hybrid seed. In particular, they may be used to drive the pollen-specific
 CC expression of heterologous genes which confer nuclear or cytoplasmic male
 CC sterility in transgenic plants (e.g., cereals). The present sequence
 CC represents a ZMMADS2 gene 3' regulatory element.

Sequence 251 BP; 81 A; 27 C; 61 G; 82 T; 0 other;

Query Match

Best Local Similarity 13.6%; Score 174.4; DB 22; Length 251;
 Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1083 agaagagtaaaactgcgcgttctatgatgtgaagaaactatttgaagagatgat 1142
 Db 1 agaaagataaaactgcgcgttctatgatgtgaagaaactatttgaagagatgat 60
 QY 1143 actcagagaaagacatatttggcgagagattgagatagaaactataatgtatg 1202
 Db 61 actcagagaaagacatatttggcgagagattgagatagaaactataatgtatg 120
 QY 1203 caataatttccagaccggaatgggtcgtggaattcagaagatgattgcttcta 1258
 Db 121 caataatttccagaccggaatgggtcgtggaattcagaagatgattgcttcta 176

RESULT 14

AAAF76454
ID AAF76454 standard; DNA; 251 BP.

AAAF76454;

11-MAY-2001 (first entry)

Maize ZMMADS2 gene fragment SEQ ID NO: 11.

KW Male sterile plant; maize; hybrid breeding; pollen tube; ZMMADS2;
 KW grain; cereal; corn; ds.

OS Zea mays.

WO200112798-A2.

22-FEB-2001.

16-AUG-2000; 2000WO-EP08001.

18-AUG-1999; 99EP-0116267.

(SUED-) SUEDEWESTDEUTSCHE SAATZUCHT.

Loerz H, Dresselhaus T, Schreiber D, Heuer S;

WPI: 2001-211213/21.

Novel nucleic acid molecule, ZMMADS2 derived from pollen of Zea mays
 useful for cloning and expressing a pollen specific sequence in a plant
 and for producing male sterile plants -
 Claim 2; Page 70; 76pp; English.

CC The present invention provides the protein and coding sequences of the
 CC Zea mays ZMMADS2 protein, which is specifically expressed in pollen. The
 CC sequences can be used to produce male sterile plants, as ZMMADS2 is
 CC essential for pollen tube growth. These are useful in hybrid breeding,
 CC particularly of corn, cereal and grain. The present sequence is part of
 CC the ZMMADS2 coding sequence.

Sequence 251 BP; 81 A; 27 C; 61 G; 82 T; 0 other;

Query Match	13.68;	Score 174.4;	DB 22;	Length 251;
Best Local Similarity	99.48;	Pred. No. 6.6e-37;		
Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

RESULT	15
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ID	AAA99364 standard; DNA; 909 BP.
XX	

QY 360 atgggagggaaagatcgtgatccgcagatcgataactccaagagccgcgcagtgacc 419

Db	1	atggctcg tgggaagattgagataaaggaggttgaataactaagaacgcagctaac	60
Qy	420	ttctccaagcgccggaaacgggatacttcaagaagccaaaggagctgcacactcgtcat	479
Db	61	tcttcgaagcgccgaaatggtttattaagaagaagcgatataatcatctcttggat	120
Qy	480	ggcgaaagtcgcgcctgcatacttctccaagcccgccgcctcagtgactcagacc	539
Db	121	gaaagaagcgccccaatcgcgtctctccaagcgaggaggaactttagaatttgcacaccac	180
Qy	540	agcatgaataatcagtlatacgcgttacgcgaagc---caagagaagcgcaagctgcgc	596
Db	181	agcgtgaagagagacgatttgagtgacaagaagccttgcgttgcacaacaacgaagggg	240
Qy	557	gcaaatcccaactcggagcttaagttttggcaaaaggagcgcaagccttgagacaaca	656
Db	241	ggcatatacgaagctccaacttcacgatttggcaacaagaagcctgttlaactcagacaacag	300
Qy	657	ctgcgaactctgcgaanaaatatcagcgcaagtgcggagatgattcttccttgagctaat	716
Db	301	attcacattttgcgaataatgcacaataagcatttgcgttgagcgggtcttaacgcttgaac	360
Qy	717	gtcaagaagactgcagctccctgcgaagaatccaatttgaanaaacaagccgcgtgtgtccgcga	776
Db	361	attaagaagaccgaagcaacttgaggtctcgacttgaanaaaggaaatcacgcgaugcgatcc	420
Qy	777	aagaagagacatctcttgatagatgagatllcaacgatttgaatcgaagaagcaatttat	836
Db	421	aaaaagaacgagatgctgttcgaagagatcgacatcatcagacagaaaggaacacatactt	480
Qy	837	caccaagaataatcacagacttgtaacaataagat	868
Db	481	atccagaagaaatgagatcttcgcgaacaagat	512

Search completed: August 11, 2002, 08:42:14
Job time: 4354 sec

Mon Aug 12 08:29:58 2002

us-09-970-624-1.rng

Page 16

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 05:49:44 ; Search time 49.52 Seconds
(without alignments)
6349.170 Million cell updates/sec

Title: US-09-970-624-1

Perfect score: 1280
1 gcaagagccgcctgcgcga.....aaaaaaaaaaaaaaaaaaaa 1280

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.NA: *
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165.8	13.0	1043	2	US-08-867-087B-12
2	149.4	11.7	1141	2	US-08-323-449B-1
3	149.4	11.7	1141	2	US-08-485-981-1
4	149.4	11.7	1141	2	US-08-867-087B-1
5	147.8	11.5	1125	1	US-08-460-512-6
6	142.4	11.1	1457	1	US-08-460-512-1
7	142.2	11.1	959	4	US-09-067-800-7
8	142.2	11.1	959	4	US-09-349-677-7
9	140.8	11.0	1097	1	US-08-460-512-3
10	133.6	10.4	1345	1	US-08-592-214A-7
11	133.6	10.4	1345	3	US-08-659-188-7
12	133.6	10.4	1345	3	US-08-655-227-7
13	133.6	10.4	1345	3	US-08-655-241-7
14	133.6	10.4	1345	3	US-09-149-976-7
15	133.6	10.4	1345	3	US-09-398-326-7
16	129.4	10.1	1027	2	US-08-867-087B-54
17	127.8	10.0	1180	2	US-08-867-087B-16
18	123.8	9.7	896	4	US-09-067-800-5
19	123.8	9.7	896	4	US-09-349-677-5
20	114	8.9	1059	2	US-08-867-087B-14
21	109.6	8.6	945	2	US-08-485-981-9
22	109.6	8.6	945	2	US-08-867-087B-10
23	105.4	8.2	795	3	US-08-904-284-2
24	101	7.9	6138	4	US-09-067-800-4
25	101	7.9	6138	4	US-09-349-677-4
26	95.8	7.5	1500	5	PCT-US93-08386-3
27	95	7.4	1062	4	US-09-067-800-1

28	95	7.4	1062	4	US-09-105-652-1	Sequence 1, Appli
29	95	7.4	1062	4	US-09-349-677-1	Sequence 1, Appli
30	91.6	7.2	2679	3	US-08-904-284-4	Sequence 4, Appli
31	91.4	7.1	5622	4	US-09-067-800-3	Sequence 3, Appli
32	91.4	7.1	5622	4	US-09-349-677-3	Sequence 3, Appli
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34	90.2	7.0	756	1	US-08-592-214A-11	Sequence 11, Appli
35	90.2	7.0	756	3	US-08-655-188-11	Sequence 11, Appli
36	90.2	7.0	756	3	US-08-655-227-11	Sequence 11, Appli
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38	90.2	7.0	756	3	US-09-149-976-11	Sequence 11, Appli
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43	89.4	7.0	779	3	US-08-655-241-9	Sequence 9, Appli
44	89.4	7.0	779	3	US-09-149-976-9	Sequence 9, Appli
45	89.4	7.0	779	4	US-09-398-326-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-867-087B-12
; Sequence 12, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist, LLP
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; City: Portland
; State: Oregon
; Country: United States of America
; Zip: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1043 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-867-087B-12
Query Match 13.0%; Score 165.8; DB 2; Length 1043;

Query Match	11.7%	Score 149.4	DB 2	length 1141
Best Local Similarity	57.8%	Pred. No. 4,4e-31		
Matches 344	Conservative 0	Mismatches 241	Indels 10	Gaps 4
QY	300	taagctgtcaagcgcgcagccaggtlccaagaagaagctagctatagctacgcgcgaatcg	359	
Db	6	TACCTTGCAAGGCGCATGACTAGTAGAGACGAGAGAGAGAGAGAGAGAGAGAA	64	
QY	360	atggggaggggaaagaatcgtagtccgcagagatcgataactccacgcagcgcgagctgacc	419	
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QY	420	ttctccaagcgcgcgcgaacgcggaattcttcaagaagaccgaagagctgcgcattcccttcgcat	479	
Db	125	TTTCGCCAAGGCGAGAACGGCTCGTCACAAGAGCCTTCAGGCTCTCCCTCTCTCGGAC	184	
QY	480	gcggaggtcgcgctcgtaattcttccagacgcgcgcgcgcgcctctacgaagtactagc--	536	
Db	185	GCGGAGGTGCGCCCTCATCATCTTCTCCGCGCGCGCGCCCTCTCGAGTTCCTCAGGTCA	244	
QY	537	accagatgaatatcgattagatcgtggaagcgccaagggccaaggaagagcgaatcgctc	596	

Query Match	11.78;	Score 149.4;	DB 2;	Length 1141;
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Db 202 GTTACTCAAGAAAGCTTATGAGCTCTGCTTGTGTGAGACCTAGGTGTCTTGTCA 261
QY 499 tcttccagaccgcccgtctcagagtaactagacacgaatgaatcagttatag 558
Db 262 tcttccagaccgcccgtctcagagtaactagacacgaatgaatcagttatag 321
QY 559 atcgtacagcgaagc---caaggaagagcagcagctcgtcgaatcccaactcgcgc 615
Db 322 AAAGGTACAGAAAGCTTGTCTCCGACGCCGTTAACCTCCGACATCCGACATTCAGATT 381
QY 616 ttaagtttggcaaaaggagcagcagcttgaagacaaactgacacttgaagaana 675
Db 382 CTCACACTACTATCAGCAAGAGGCGTCTAAACCTCCGACAGACATTCGACATTCAGATT 441
QY 676 attatcgagcagttgacggaatgaatgacttcttgagctgaatgaatgaatcgcgc 735
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QY 736 tggagaatcaattggaacaagcctgcgtggtgctcgcgaagaagaagacatcttga 795
Db 502 TTGAAGTAGGCTTGAGAAAGGAATCACTGCTGTCGATCCAGACAGACGACATGTTAG 561
QY 796 tagatgaattcagcagtttgaatcgaaagcagtttattcaccagaanaatacagact 855
Db 562 TTGCAGAGATTGAATATCATGCAAAAAGGAATCATGACCTGCAAAACGATATGATC 621
QY 856 tgaacaataagatca 870
Db 622 TCCGCTCCAGATTGA 636

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RESULT 8

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US-09-349-677-7
; Sequence 7, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 959 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 78..818
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..959
; OTHER INFORMATION: /note="AGL5 cDNA and deduced
; OTHER INFORMATION: protein sequences."
; US-09-349-677-7

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Query Match 11.1%; Score 142.2; DB 4; Length 959;
Best Local Similarity 54.8%; Pred. No. 3.6e-29;
Matches 304; Conservatve 0; Mismatches 248; Indels 3; Gaps 1;

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QY 319 aggtcagaagagagctagctagctatagccggagatcgatgggagggagaatcgc 378
Db 82 AGGGTGGTGGAGTATGAAATGACAGAGACGCAAGAAGATAGGAGAGGAAATAG 141
QY 379 tgaatcgagatcgatgaatcctcagcagcgcaggtgacatctccaaagcgcggaac 438
Db 142 AGATTAAGAGAGATGAGAAACACTACGAATCGTCAACTTCTTCCAAACGACGCAATG 201
QY 439 ggaatcgaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 498
Db 202 GTTACTCAAGAAAGCTTATGAGCTCTGCTTGTGTGACGCTGAGGTTGCTTGTCA 261
QY 499 tcttccagaccgcccgtctcagagtaactagacacgaatgaatgaatcagttatag 558
Db 262 TCTTCCCACTGAGGCCGCTCTTCTAGATGACGCCAACAACAGTGTGAGAGAAATAG 321
QY 559 atcgtacagcgaagc---caaggaagcagcagcagcagcagcagcagcagcagcagc 615
Db 322 AAAGGTACAGAAAGCTTCTCCGACGCCGTTAACCTCCGACATCCGACATTCAGATT 381
QY 616 ttaagtttggcaaaaggagcagcagcagcagcagcagcagcagcagcagcagcagcagc 675
Db 382 CTCACACTACTATCAGCAAGAGGCGTCTAAACCTCCGACAGACATTCGACATTCAGATT 441
QY 676 attatcgagcagttgacggaatgaatgacttcttgagctgaatgaatgaatcgcgc 735
Db 442 TGAACAGACACACTTCTTGTGTAATCTTGTCTTCTTGAACCTTGAAGAACTCAAGAAC 501
QY 736 tggagaatcaattggaacaagcctgcgtggtgctcgcgaagaagaagacatcttga 795
Db 502 TTGAAGTAGGCTTGAGAAAGGAATCATGCTGCTCCGATCCAGAAAGCAGGATGTTAG 561
QY 796 tagatgaattcagcagtttgaatcgaaagcagtttattcaccagaanaatacagact 855
Db 562 TTGCAGAGATTGAATATCATGCAAAAAGGAATCATGACCTGCAAAACGATATGATC 621
QY 856 tgaacaataagatca 870
Db 622 TCCGCTCCAGATTGA 636

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RESULT 9

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US-08-460-512-3
; Sequence 3, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOSKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Treceartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California

```

COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,512
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/293,278
FILING DATE:
APPLICATION NUMBER: US/07/956,694
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RET
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1097 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 126..884
US-08-460-512-3

Query Match 11.0%; Score 140.8; DB 1; Length 1097;
Best Local Similarity 57.0%; Pred. No. 9.2e-29;
Matches 278; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

QY 363 gggaggggaaagatcgtgatccgcagagatcgaactcgaagccgcgagtgaccttc 422
DB 177 GGGAGAGGAAAGATCGAATAAAGCGATCGAGAACACACACGCCGTCAGATTCTTC 236
QY 423 tccaagcgccggaacgagatcttcaagaagcgcaagcgatcgccatctctgagatcg 482
DB 237 TCGAAGCGGAGAAATGCTTGTCTCAAGAAAGCTTACGAATCTCTGTTCTTTGTATCCT 296
QY 483 gaggtcgctcgtcatcttctccagcagcgccgctctacgagtgactctagcaccagc 542
DB 297 GAAGTCGACATCTGTTCTTCTTCTAGCGCGTGGCGTCTCTTATGACTACTCAACAAGT 356
QY 543 atgaatcagttatagatcgtgtaagcgcaagcgaagcgcaagcgcaagcgcaagcgca 599
DB 357 GTAAAAAGGACAAATGAGAGGTAAGAAAGCAATATCGAATATCTTAACACCGATCC 416
QY 600 aatcccaactcgagcgttaagtttggcaagggagcgcaagcgttgagacaactcg 659
DB 417 GTGGCAGAAATTAATGACAGATATTAATCAACAAGATCTGCCAATTTGCGTCAACAATT 476
QY 660 cacaacttgcagaagaatataatcgcgagttgacgagagatgactcttctggtgtaatg 719
DB 477 ATCAGCATACAGAACTCGAAGCAGCAATGATGAGTGGTGAAGCATGTCATGTCCTCC 536
QY 720 aaagacatgcagtccttgagagataaalttggaaacaagcgtggtggtgcgcgcaag 779
DB 537 AAAGAGCTCAGAACTTGGAAAGGCAAGATTAGACAGAAAGTTAAATCGAATCGATCCAG 596
QY 780 aaggacatctctgtagatagatcaggaattggaatcgaaagcgaagttatctac 839
DB 597 AAGAACGAACCTTATTCGCCGAATTAATGACTATGATGACAGAGAGAAAGTTGATTTGCAT 656
QY 840 caagaana 847

DB 657 AACGATAA 664
RESULT 10
US-08-592-214A-7
Sequence 7, Application US/08592214A
Patent No. 581536
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
NUMBER OF INVENTION: Genes and Methods of Using Same
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays Api"
US-08-592-214A-7

Query Match 10.4%; Score 133.6; DB 1; Length 1345;
Best Local Similarity 57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;

QY 348 ggcgcgagatcgtatgggggaggggaaagatcgtgatccgcagagatcgttaactccagagc 407
DB 137 GCGCAACAGCGGATGGGCGCGCAAGCTACAGCTGAAGCGGATAGGAACAAGATTAAC 196
QY 408 cggagtgacctcttccaaagcgccggaacgagatcttcaagaagcgcaagagatcgcc 467
DB 197 CGGCAAGGAGACTCTCTCAAGCGCGGAGACGCGCTGCTCAAGAAAGCGCACAGATCTCC 256
QY 468 atcctctgagtcgagagtgctgcctcgtcatcttctccagcagcgccgctctacgag 527
DB 257 GTCTCTGCGATGCCGAGGTCGCGTATGCTTCTCCCAAGGCGCAAGCTCTACGAG 316
QY 528 tactcta---gcaccaatgaatcagttatagatcgtgtaagcgcaagcgcaagagag 584
DB 317 TAGCCACCGCATCCCGCATGACAAAATTTGAAACGCTATGACGATATTCCTATGCTP 376

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = zea mays Apl. "
US-08-655-227-7

Query Match 10.4%; Score 133.6; DB 3; Length 1345;
Best Local Similarity 57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;

QY 348 ggcgcgagatcgatgggaggggaaagatcgtgctccgagatcgatccagcagc 407
DB 137 GGCACACAGGCGATGGGCGCGGACGTACAGCTGAAGCGATAGAACACAGATAAC 196
QY 408 cgcgagtgacctctcccaagcgcgcggaacggaatcttcaagaagcgaagagctcgc 467
DB 197 CGCAGAGTACTTCTCCAAAGCGCGGAGCGCTGCTCAAGAGGCGGACAGATCTCC 256
QY 468 atccctgagatgcggaagtcgcgcctgcatctctccagaccgcgcctctacgag 527
DB 257 GTCTCTGCGATGCGGAGGTCGCGCTCATCTCTTCCCGCCAGAGCGCAACCTCTAGAG 316
QY 528 tactcta---gcaccagatgaatcagttatagatcgatcggaagcgcaagaagag 584
DB 317 TACGCCACCGACTCCCGCATGACAAATTTCTGAACCGCTATGAGCATATTCCTATGCT 376
QY 585 cagcaagtcgctgcgaatcccaactcgcgaagcttaagt-----ttggcaagggagagc 640
DB 377 GAAGAAGCTCTTATTTCAGCTGAATCTGAAGTGAGGGAATTTGGTCCACAGATACAGG 436
QY 641 aagcttgacaacaactgcgaacttgcgaagaataattatgcgaagttgcgagatga 700
DB 437 AAACCTGAAGGCCAAATTTG-AGACCATACAAATAATGCCACAGCACTGATGGGAGAGA 495
QY 701 tcttctgagtgatgaatgcgaagaactcagtcctgaggaatcaattggaaacaagct 760
DB 496 TCTAGAGCTTTGAATCCCAAGAGAGCTCCAGCACTAGAGCAAGCTGATGCTACT 555
QY 761 gcggtggtgcgcgcaagaaggaagaccatctctgtatagatgagatltcaagatcg 820
DB 556 GAAGCACAATCAGATCAAGAGAGAGCCACTTATGCGGAGTCTATTCTGAGCTACAGAA 615
QY 821 aaagcaagttatttaccacaagaataacagactgttaca 862
DB 616 GAAGGAGAGCTACTGCAAGAGAGAGACAAAGCTCTGAGAA 657

RESULT 13

US-08-655-241-7
Sequence 7, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigel, Detlef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays Apl. "
US-08-655-241-7

Query Match 10.4%; Score 133.6; DB 3; Length 1345;
Best Local Similarity 57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;

QY 348 ggcgcgagatcgatgggaggggaaagatcgtgctccgagatcgatccagcagc 407
DB 137 GGCACACAGGCGATGGGCGCGGACAGTACAGCTGAAGCGGATAGAGAAACAGATAAC 196
QY 408 cgcgagtgacctctcccaagcgcgcggaacggaatcttcaagaagcgaagagctcgc 467
DB 197 CGCAGAGTACTTCTCCAAAGCGCGGAGCGCTGCTCAAGAGGCGGACAGATCTCC 256
QY 468 atccctgagatgcggaagtcgcgcctgcatctctccagaccgcgcctctacgag 527
DB 257 GTCTCTGCGATGCGGAGGTCGCGCTCATCTCTTCCCGCCAGAGCGCAACCTCTAGAG 316
QY 528 tactcta---gcaccagatgaatcagttatagatcgatcggaagcgcaagaagag 584
DB 317 TACGCCACCGACTCCCGCATGAGCAAAATTTCTGAACCGCTATGAGCATATTCCTATGCT 376
QY 585 cagcaagtcgctgcgaatcccaactcgcgaagcttaagt-----ttggcaagggagagc 640
DB 377 GAAGAAGCTCTTATTTCAGCTGAATCTGAAGTGAGGGAATTTGGTCCACAGATACAGG 436
QY 641 aagcttgacaacaactgcgaacttgcgaagaataattatgcgaagttgcgagatga 700
DB 437 AAACCTGAAGGCCAAATTTG-AGACCATACAAATAATGCCACAGCACTGATGGGAGAGA 495
QY 701 tcttctgagtgatgaatgcgaagaactcagtcctgaggaatcaattggaaacaagct 760
DB 496 TCTAGAGCTTTGAATCCCAAGAGAGCTCCAGCACTAGAGCAAGCTGATGCTACT 555
QY 761 gcggtggtgcgcgcaagaaggaagaccatctctgtatagatgagatltcaagatcg 820
DB 556 GAAGCACAATCAGATCAAGAGAGAGCCACTTATGCGGAGTCTATTCTGAGCTACAGAA 615
QY 821 aaagcaagttatttaccacaagaataacagactgttaca 862
DB 616 GAAGGAGAGCTACTGCAAGAGAGAGACAAAGCTCTGAGAA 657

RESULT 14
US-09-149-976-7
Sequence 7, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
City: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
NAME/KEY: misc.feature
LOCATION: 1..1345
OTHER INFORMATION: /note="product = Zea mays APl"
US-09-149-976-7

Query Match 10.4%; Score 133.6; DB 3; Length 1345;
Best Local Similarity 57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;
QY 348 ggcgcgaagatcgatgggaggaagatcgatgcgacgaagatcgataactccacgagc 407
DB 137 ggcgaacaaagcgtggggcgacgaagctgaacgagatagagaaacaaagtaaac 196
QY 408 cgcgaagtgacctcttcacgaagcgcgaagcgaagatcttaagaagccaaagagctgcgc 467
DB 197 cgcgaagtgacctcttcacgaagcgcgaagcgaagatcttaagaagcgcgaagatctgc 256
QY 468 atccctcgatcgagagatcgagcctcgatcactcttcacgaagcgcgcgcctcgaag 527
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QY 528 tactcta---gcaccgaatgaatcagttatagatcggtacgcaagcgaaggaagag 584
DB 317 TAGGCACGACGACTCCCGCATGAGCAAAATTTTGAACGCTATGACGATATTCCTATGCT 376
QY 585 cagcaagtcgtcgcaaatcccaatcgcgaagcctaagc-----ttggcaaggaagcagc 640

DB 377 GAAAAGGCTCTTATTTCAGCTGATCTGAAGTGAAGGGAATTTGGTCCACGATATACAGG 436
QY 641 aaagcttgagacaacaactgcacacttgcagaanaattatcgcaagttgcagcgagatga 700
DB 437 AAACCTGAAGGCCAAATTTG-AGACCATACAAAAATGCCACAAGCACCTGATGGAGAGGA 495
QY 701 tcttcctggcgtgaatgcagaagactcagtccttcgagagatcaattggaacaagcct 760
DB 496 TCTTAGAGCTTTGAAATCCCAAGAGCTTCAGCACTAGAGCAGCAGCTGATAGCTACT 555
QY 761 gctgtgtcgcgcgaagaagacatctcttgaatagatagattcaagattgaatcg 820
DB 556 GAAGCAGATCAGATCAAGAGAGAGCCACTTATGGCCGAGTCTATTCTTGAGCTACAGAA 615
QY 821 aaagcaagttatttcccaagaanaataacagacttgaaca 862
DB 616 GAAGGAGAGGTCACTCGAGAGAGAGAACAGGCTCTGACGAA 657

RESULT 15
US-09-398-326-7
Sequence 7, Application US/09398326
Patent No. 6355863
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
City: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
NAME/KEY: misc.feature
LOCATION: 1..1345
OTHER INFORMATION: /note="product = Zea mays APl."
US-09-398-326-7

Query Match 10.4%; Score 133.6; DB 4; Length 1345;

Best Local Similarity 57.58; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;

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OY	408	cggcagatgtaccttcctccaaagcgccggaacggatctctcaaaagagccaaagagctcgcc	467
Db	197	CGCGAGGAGACTCTTCCAAACGCCGGAAACCGCCTGCTCAAGAGGCGCACAGATCTCC	256
OY	468	atccctctcgaatgcgaagatcgccctgcgtacatctctccagacacggcgccctcagag	527
Db	257	GTCTCTTCGATGGCGAGAGTGGCCGTATCGTCTTCTTCCCCCAAGGCAAGCTCTACGAG	316
OY	528	tactctc---gcaccagatgaatcagttatagatcgtacgcaagcgccaaagaaag	584
Db	317	TACGCGACCGACTCCCGGATGAGCAAAAATCTTGAAAGGCTATGAGCATTTCTCTATGCT	376
OY	585	cagcaagtcgcgcgaataatcccaactcggagcttaagc-----ttggcaagggagagcagc	640
Db	377	GAAGAAGCTCTTATTTCAGCTGGAATTCGAAATGAGGAAATTGGTCCACGAAATTCAGG	436
OY	641	aagcttgaacacaactgcacaacttgcagaanaattalcggaattgcacggagatatga	700
Db	437	AAACTGAAGGCGCAAAATTTG-AGACCATACAAAAATGCCACAGACACTGATGGGAGGGA	495
OY	701	tcttctcgtgagctgaatgtcaaaagactcgagctccctctggaataatccaattgaaacaagcct	760
Db	486	TCTAGAGCTTTGAAATCCCAAGAGGCTCCAGCAACTGAGACACACGCTGGATAGCTCAGT	555
OY	761	gcgttgtgtgccgcgcaaaagaagacacatctcttgatagatcgagatcaacatttgaatcg	820
Db	556	GAAAGCATCTAGATCCAAAGAAAGAGACCCTTATGCGCGAGTCTATTTCAGCTACAGAA	615
OY	821	aaagcgaaattatttcaaccaagaanaatacaagactgttaca	862
Db	616	GAAAGAGAGTCACTCGACGAGGGAACAAGGCTCTTCACAA	657

Search completed: August 11, 2002, 08:38:22
Job time: 10118 sec

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5

6

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 05:46:56 ; Search time 1691.01 Seconds
(without alignments)
10216.440 Million cell updates/sec

Title: US-09-970-624-1

Perfect score: 1280

Sequence: 1 gacagcagccgcctgcgcga.....aaaaaaaaaaaaaaaa 1280

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
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15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569.4	44.5	614	9	AW453286 660039F01
2	544.6	42.5	608	9	AW067614 61404610
3	377.6	29.5	434	9	AI947410 61404610
4	333.2	26.0	468	9	AW053261 614073H05
5	269	21.0	463	10	BE354988 614073H05
6	263.6	20.6	716	10	BM405213 EST579540
7	253	19.8	632	9	AM216280 EST303461
8	245	19.2	812	9	BE034403 MH04D03 M
9	245.8	19.2	553	10	BE592879 EST491557
10	237.6	18.6	487	9	AI974336 T110185e
11	236.6	18.5	499	10	BM323459 PIC1.19 E
12	230.8	18.0	581	10	BE596704 P11.58 F0
13	226	17.7	492	9	AI389596 MRC56A01
14	213.6	16.7	598	9	AW706936 SK08D08 Y
15	212.2	16.6	587	10	BE445262 WHE1133_A
16	175.4	13.7	649	9	AW184799 se82fi12.Y
17	173.6	13.6	786	9	BE195464 HVSMEH008

18	173.6	13.6	892	10	BC415259	BC415259 HVSMEK000
19	173.2	13.5	607	9	AW705451	AW705451 SK49C05.Y
20	172.8	13.5	535	9	AI995037	AI995037 701501560
21	168.2	13.1	422	10	BE341755	BE341755 EST394587
22	167	13.0	482	10	BE319808	BE319808 NF020A03R
23	166.6	13.0	698	10	BE659915	BE659915 7-H4 Gmax
24	165.8	13.0	507	10	BE319610	BE319610 NF015605R
25	165.4	12.9	455	10	BC651806	BC651806 sad61C04
26	163.8	12.8	558	9	AW705787	AW705787 SK51H05.Y
27	163.4	12.8	608	9	AW278878	AW278878 sf99h09.Y
28	162.8	12.7	493	10	BE423660	BE423660 WHE0072_B
29	162.8	12.7	597	9	AW704750	AW704750 SK35A06.Y
30	161.4	12.6	543	10	BE659914	BE659914 4-C1 Gmax
31	160.6	12.5	613	10	BE659913	BE659913 3-D9 Gmax
32	159.4	12.5	804	10	BC414586	BC414586 HVSMEK000
33	157.4	12.3	960	10	BC445265	BC445265 GA_Ea002
34	156.2	12.2	863	10	BI958127	BI958127 HVSMEH001
35	155.6	12.2	700	9	AL509053	AL509053 AL509053
36	155.2	12.1	566	9	AI728519	AI728519 BN1GH1109
37	154.8	12.1	872	10	BE456120	BE456120 HVSMEG001
38	154.6	12.1	726	10	BE430838	BE430838 SUN006.D0
39	154.2	12.0	481	10	BE610259	BE610259 sg52a10.Y
40	154.2	12.0	700	9	AL506480	AL506480 AL506480
41	154	12.0	584	10	BC442607	BC442607 GA_Ea001
42	153.6	12.0	512	10	BC367358	BC367358 HVSME1001
43	153.6	12.0	561	10	BM324399	BM324399 PIC1.27_G
44	152.8	11.9	754	10	BI311053	BI311053 EST531280
45	152.8	11.9	916	10	BE454527	BE454527 HVSMEH009

ALIGNMENTS

RESULT 1
AW453286 660039F01.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
LOCUS mRNA sequence.
DEFINITION
ACCESSION AW453286.1 GI:6994072
VERSION
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE 1 (bases 1 to 614)
AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford University
TITLE Walbot,V.
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 660039 row: F column: 01.
Location/Qualifiers
1. 614
/organism="Zea mays"
/cultivar="Ohia43"
/db_xref="taxon:4577"
/clone_lib="660 - Mixed stages of anther and pollen"
/tissue_type="whole premeiotic anthers to pollen shed"
/dev_stage="premeiotic anthers to pollen shed"
/lab_host="XLR"
/note="Organ: anthers; Vector: Lambda Zap; Site:1; EcorI; Site:2; XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcorI site. Created by Amie Franklin."

BASE COUNT 213 a 113 c 139 g 149 t

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 434)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614044 row: G column: 10.
Location/Qualifiers

FEATURES
source

1. .434
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="X10LR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"

BASE COUNT 123 a 95 c 69 g 145 t 2 others
ORIGIN

Query Match 29.5%; Score 377.6; DB 9; Length 434;
Best Local Similarity 98.4%; Pred. No. 5.8e-52;
Matches 380; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 873 ctgattcgccaaagaatgatgattacataaaagatatatgagactgaagaccaggt 932
DB 434 ctgattcgccaaagaatgatgattacataaaagatatatgagactgaagaccaggt 375
QY 933 ggaattatcgagagtcacgcagctccatcgaacttgcagtgatgtaaacagagatgtt 992
DB 374 ggaattatcgagagtcacgcagctccatcgaacttgcagtgatgtaaacagagatgtt 315
QY 993 cctgtgcaacttgaactgacacactgcagcagcaaaataacatgagccatctactgt 1052
DB 314 ccaagtcgaacttgaactgacacactgcagcagcaaaataacatgagccatctactgt 255
QY 1053 cctaaagctagattgcaattatccatgaagaagatlaaaactgcgctctatgatgt 1112
DB 254 cctaaagctagattgcaattatccatgaagaagatlaaaactgcgctctatgatgt 195
QY 1113 gaaggaactattatctgtgaagagatgactcagagaagaacatatttgcgagaga 1172
DB 194 gaaggaactattatctgtgaagagatgactcagagaagaacatatttgcgagaga 135
QY 1173 gatttaagatgaacttataatgaatgaactaatttcagaccggaatggagtcgt 1232
DB 134 gatttaagatgaacttataatgaatgaactaatttcagaccggaatggagtcgt 75
QY 1233 ggaatcagaagatgattgcttcta 1258
DB 74 ggaatcagaagatgattgcttcta 49

RESULT 4
AM053261 468 bp mRNA linear EST 20-SEP-1999
LOCUS 614073H05.x1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AM053261
VERSION AM053261.1 GI:5915620
KEYWORDS EST.
SOURCE Zea mays.

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 468)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614073 row: H column: 05.
Location/Qualifiers

FEATURES
source

1. .468
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="X10LR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"

BASE COUNT 139 a 102 c 77 g 148 t 2 others
ORIGIN

Query Match 26.0%; Score 333.2; DB 9; Length 468;
Best Local Similarity 98.5%; Pred. No. 9.4e-45;
Matches 335; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 919 ctgaagaccagaagtgagtgtaactcgaggagtcacccagactcattcagtgatgag 978
DB 468 ctgaagaccagaagtgagtgtaactcgaggagtcacccagactcattcagtgatgag 409
QY 979 aaaccagagatgtctcgtgtgcaacttgaactcagacacgtgcagcaaaataacatg 1038
DB 408 aaaccagagatgtctcgtgtgcaacttgaactcagacacgtgcagcaaaataacatg 349
QY 1039 agccatcactgcctcctaagtagattgcaattatccatgaagaagatlaaaactgc 1098
DB 348 agccatcactgcctcctaagtagattgcaattatccatgaagaagatlaaaactgc 289
QY 1099 cgtctatgatgctgaaagaactattatgtgaagaagatgactcagagaagaagat 1158
DB 288 cgtctatgatgctgaaagaactattatgtgaagaagatgactcagagaagaagat 229
QY 1159 atttgtgcaagagatttgagatatgaacttaaatgtatgaatgaatatttcagac 1218
DB 228 atttgtgcaagagatttgagatatgaacttaaatgtatgaatgaatatttcagac 169
QY 1219 cggaaatgggtcgtggaattcagagagatgcttctcta 1258
DB 168 tggaaatgggtcgtggaattcagagagatgcttctcta 129

RESULT 5
BE354988 463 bp mRNA linear EST 20-JUL-2000
LOCUS BE354988
DEFINITION DGI_10.H09.b1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION BE354988
VERSION BE354988.1 GI:9296098
KEYWORDS EST.
SOURCE Sorghum bicolor
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade: Panicoidae; Andropogoneae; Sorghum.
 1 (bases 1 to 463)
 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
 L.H.
 An EST database from Sorghum: dark-grown seedlings
 unpublished (2000)
 Contact: Cordonnier-Pratt MM
 Department of Botany
 The University of Georgia
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 542 1805
 Email: mmp@prattuga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: JEN REV
 High quality sequence stop: 461
 POLYA-No.

FEATURES
 source
 Location/Qualifiers
 1..463
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 /clone_lib="Dark Grown 1 (DG1)"
 /note="Organ: 5-day-old dark-grown seedlings; Vector:
 lambda Zap; Site 1: XhoI; Site 2: EcoRI; The library was
 made from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision."
 BASE COUNT
 112 a 125 c 138 g 88 t
 ORIGIN

Query Match 21.0%; Score 269; DB 10; Length 463;
 Best Local Similarity 85.7%; Pred. No. 2.5e-34;
 Matches 299; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 349 gccgagatcgtgagaggaagatcgtatccgacgacgataactccagagcc 408
 114 GCTTGACGACGATGGGGCGGCAAGATGATGATCCCGGATGACACTCCGAGGCC 173
 QY 409 ggcaggtgacctctccaaagccggaagagatcttcaagaagccaagagatcgca 468
 174 GCGAGGTGACGTCTCCAAAGCGGGAAGGATCTTCAAGAAAGCAAGAGAGCTCGCA 233
 QY 469 tccctcgatgagagagtcgctcgtcatctctccagacgagcgccctcaagat 528
 234 TCCCTGTGATCGGAGAGTGTGATGATCTTCTCCAGCAGCGGCTCTACGAAAT 293
 QY 529 actctagaccagcagatgaatcagttatagatcgtagcgaagccaagagaagcagc 588
 294 ACCGACAGACAAAGCATGAAGTCAATGATGATGTCGAGCAAGAGAGAGCAGC 353
 QY 589 aagtcgtcgcaaatcccaactcgaagcttaagtttggcaaaaggaagcgaagcttga 648
 354 AGCTTTGAGCAAAACCAACACAGAACTTAAGTTCTGGCAAAAGGAGCAAAAGCTTGA 413
 QY 649 gacacacactgacacactgcaaaataatatacgacagttgacgagaga 697
 414 GACAAACAACCTGCACAACTTGCAAGAAATATCATCGCAGTTGATGGGACA 462
 Db

RESULT 6
 BM405213 716 bp mRNA linear EST 22-JAN-2002
 LOCUS EST579540 potato roots Solanum tuberosum cDNA clone cPR02019 5'
 DEFINITION end, mRNA sequence.
 ACCESSION BM405213
 VERSION BM405213.1 GI:18256723
 KEYWORDS EST.
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 716)
 van der Hoeven, R., Sun, H., Karameycheva, S.A., Tsai, J., Van Aken, S.,
 Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,
 Tankley, S. and Baker, B.
 Generation of ESTs from potato roots
 unpublished (2001)
 Contact: Research Genetics, Libraries Division
 Tel: 1-800-711-6195
 Email: cdna@resgen.com
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdna@resgen.com
 Seq primer: T3.

FEATURES
 source
 Location/Qualifiers
 1..716
 /organism="Solanum tuberosum"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cPR02019"
 /clone_lib="potato roots"
 /tissue_type="roots"
 /dev_stage="in vitro grown stem cuttings"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Cornell University, Tankley lab;
 sequencing: The Institute for Genomic Research. Roots were
 isolated from in vitro grown stem cuttings on CM medium.
 Roots were isolated two weeks after placing the stem
 cuttings from in vitro grown plants on medium."
 BASE COUNT
 256 a 125 c 172 g 163 t
 ORIGIN

Query Match 20.6%; Score 263.6; DB 10; Length 716;
 Best Local Similarity 69.8%; Pred. No. 1.8e-33;
 Matches 356; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
 QY 357 tcatgaggagaggaagatcgtatccgacgacgataactccagagccgagatg 416
 56 TAGATGGAAAGGGAAGATGATGATCGAAGATGATGATCAACGAACGCAATTT 115
 QY 417 acccttccacgc 476
 116 ACTTCTCAAGAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 175
 QY 477 gatcgagagtcgctcgtcatctctccagaccgcgcgcgcgcgcgcgcgcgcgcgc 536
 176 GATGCTGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 235
 QY 537 accagatgaatcagttatagatcgtagcgaagccaagagaagcagaagtcgtc 596
 236 ACCAGATGAATCACTTATTACGATACACCAAAACGAAGAGAGATTTGACGAATTG 295
 QY 597 gcaatcccaactcgaagcttaagtttggcaaaaggaagcgaagcttgaagacaa 656
 296 CACAAATCCAGTGTCAAGAACTCAAGCTGTGGCAGAGGAGGACGAGATCTTGGGCAACAA 355
 QY 657 ctgcacaactgcaagaataatatacggaagctgaagagatgatctcttgggctgaat 716
 356 CTACAGATCTGCAAGGGAATCAAGCAATATTGGAAGAGGATGATGATGATGATGAT 415
 QY 717 gtcaagaactcagtcctctgagagaatgaatgaagaacagcctcgtggtgcgcga 776
 416 GTAAAAAGAACTTAACGATCTGAGAAATCAACGTGAAGAAATGAGCTTAAGAGGATCCGATG 475
 QY 777 aagaagaccatctctctatagatagatcaagattgaatgaaaggaaggaattatc 836
 476 AAAAAGAGCAATATTGTAAGGATGAATTTCAAGAGCTAACTCGAAAGGAGGACGATATA 535
 QY 837 caccagaataatcagacttgacataag 866
 536 CATCAAGAAATTTGGAACTTCAAGAG 565
 Db

RESULT 7
 LOCUS AM218280 632 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST03461 tomato radicle, 5 d post-imbibition, Cornell University
 Lycopersicon esculentum cDNA clone cLEZ6G19 similar to Medicago
 sativa MADS-box protein, mRNA sequence.
 ACCESSION AM218280
 VERSION AM218280.1 GI:6529154
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 REFERENCE 1 (bases 1 to 632)
 van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
 Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
 Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
 Generation of ESTs from tomato radicle tissue
 JOURNAL Unpublished (1999)
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 FEATURES
 source
 1..632
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEZ6G19"
 /clone_lib="tomato radicle, 5 d post-imbibition, Cornell
 University"
 /tissue_type="radicle"
 /dev_stage="seedlings 5 days post-imbibition"
 /note="Vector: pBlueScript SK(-); Site1: EcoRI; Site2:
 XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
 (USDA-ARS, Ithaca, NY 14850)."
 BASE COUNT 192 a 112 c 171 g 157 t
 ORIGIN
 Query Match 19.8%; Score 253; DB 9; Length 632;
 Best Local Similarity 73.7%; Pred. No. 9.5e-32;
 Matches 322; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 718 tcaagaactgcagtccttgagagatcaattggaaacaagctcgtggtgctgcgca 777
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 556 TCAAGATTGGAGAACTTGGAGACCACTGGAACCACTTCGCGGTTCGTAA 615
 QY 778 agaagaccatctctg 794
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 616 GAAAGGACGAAATTCGTG 632
 RESULT 8
 BE034403 812 bp mRNA linear EST 07-JUN-2000
 LOCUS BE034403
 DEFINITION MH04D03 MH Mesembryanthemum crystallinum cDNA 5' similar to
 mads-box protein agl17-like protein, mRNA sequence.
 ACCESSION BE034403
 VERSION BE034403.1 GI:8329412
 KEYWORDS EST.
 SOURCE common ice plant.
 ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
 REFERENCE 1 (bases 1 to 812)
 Bohnerl,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,
 H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C.,
 Scara,G., Wheeler,M. and Zepeda,G.R.
 Functional genomics of Plant Stress Tolerance
 JOURNAL Unpublished (2000)
 COMMENT Contact: Michalowski,C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu
 An open reading frame exists.
 Insert length: 1 Std Error: 0.00.
 FEATURES
 source
 1..812
 /organism="Mesembryanthemum crystallinum"
 /db_xref="taxon:3544"
 /clone_lib="MH"
 /tissue_type="roots"
 /dev_stage="5-6 weeks"
 /note="grown in hydroponics, stress 400 mM NaCl (in 0.5
 Hoagland's), 78 h stress"
 BASE COUNT 263 a 176 c 168 g 193 t 12 others
 ORIGIN
 Query Match 19.2%; Score 246; DB 9; Length 812;
 Best Local Similarity 68.7%; Pred. No. 1.2e-30;
 Matches 367; Conservative 0; Mismatches 165; Indels 2; Gaps 2;

OY	658	tgcacaacttgaagaataatctggcagttgaaggaaatattcttcctggctggaag	717
Db	453	tgcacaaccttgcaaaaactcatcgacaaattatg6ggccgaamaactccttgctgaaata	552
OY	718	tcaaagaactcgaftccctcgtgagaatcaattggaacaagcctcgtgtgtgccgcga	777
Db	553	tcaaagaccatgatcattctgagAACCAACTGGAAATAGCTGGGATGAGTGCACACA	612
OY	778	agaaggaaccalcctcttgaatg-atagaattcagatttgaa-tcgaagaagcaattlact	835
Db	613	AAAAGGATCCATTGTTCCTTGATCATATCTCAAGAAGTAATAATCAATAGGCCCCATCCT	672
OY	836	tcaaccaagaanaatacagacttgtacaaataagaatcaacgcagtatgcgcaagaana	889
Db	673	GACCAAGAAGAACTGTGGAGCTGTGCATCACGCTTTAAGCTTTCGCCCCCACAAAAA	726

RESULT	9
BG592879	
LOCUS	BG592879 553 bp mRNA linear EST 12-APR-2001
DEFINITION	EST#491557 cSTS Solanum tuberosum CDNA clone cSTS2N7 5' sequence, mRNA sequence.
ACCESSION	BG592879
VERSION	BG592879.1 GI:13611019
KEYWORDS	EST.
SOURCE	Potato.
ORGANISM	Solanum tuberosum

REFERENCE
1 (phases 1 to 553)

TITLE	Generations of ESTs from sprouting potato eyes
JOURNAL	Unpublished (2000)
COMMENT	Contact: Cathy Romning

FEATURES	Location/Qualifiers
source	1. .553

BASE COUNT	163 a	106 c	144 g	140 t
ORIGIN				

Query Match	19.28;	Score 245.8;	DB 10;	Length 553;
Best Local Similarity	75.18;	Pred. No. 1.4e-30;		
Matches 307; Conservative	0;	Mismatches 102;	Indels 0;	Gaps 0

QY	Db	QY	Db
358	CGATGGGAGAGGAAAGTACTGATTAAGAGACATCGATTATTCGACGACGACAAATGA	418	CGATGGGAGAGGAAAGTACTGATTAAGAGACATCGATTATTCGACGACGACAAATGA
417	CGATGGGAGAGGAAAGTACTGATTAAGAGACATCGATTATTCGACGACGACAAATGA	477	CGATGGGAGAGGAAAGTACTGATTAAGAGACATCGATTATTCGACGACGACAAATGA
205	CGATGGGAGAGGAAAGTACTGATTAAGAGACATCGATTATTCGACGACGACAAATGA	264	CGATGGGAGAGGAAAGTACTGATTAAGAGACATCGATTATTCGACGACGACAAATGA

Accession	Gene	Protein	Length
OY	atcgagagctcgccctcgtaactctctccagacacgcgcgcctctacagtaactctgca	537	
OY	478 atcgagagctcgccctcgtaactctctccagacacgcgcgcctctacagtaactctgca	537	
Db	265 ATCGGAGGCGCGAGTACTATTTCCTTCTCCACTACTCGGAAAACCTGTATGAATATTCAGCA	322	
OY	538 ccagcataaatacgtatagatcgtgtaacygaagcccaagaaagacagctgcg	597	
Db	325 CCAGCATCAAGTCGGTGTAAAGATPACAAACAAACAAAGAGAGCAATCATCAATTGG	384	
OY	538 caaatcccaactcgagacttaagtttggcaagagggacagcaagctttagacaactaac	657	
Db	385 CAATCCCAACTCTTGAGGTATGAGTTTGGCAAAAGCGGCAATGCTAGGACAAAC	444	
OY	658 tgcacaacttgcagaataattatcgcgacttgcgagtagatgatcttcttgcgctgaatg	717	
Db	445 TACAAACTTCCAGAGATACCCGACAAATGAGGGGTGAAGACCCTTCGTGCTGTGACA	504	
OY	718 tcaagaacttcagctccctgagagatcaatttggaaacaagccttcgctg	766	
Db	505 TCMAAGATTTCAGAACTTGGAGAACCACTGGAACACGATCTTCATGG	553	

RESULT	10
LOCUS	A1974336
DEFINITION	A1974336 487 bp mRNA linear EST 26-AUG-1999 T110185e KV0 Medicago truncatula cDNA clone pV0-JJ1, mRNA sequence.
ACCESSION	A1974336
VERSION	A1974336.1 GI:5776633
KEYWORDS	EST.
SOURCE	bairrel medic.
ORGANISM	Medicago truncatula

Seq primer: SKmod (CTA gAA CTA GTg gAT CC)

FEATURES	Location/qualifiers
source	1. .487

BASE COUNT	152 a	77 c	131 g	127 t
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Query Match 18.6%; Score 237.6; DB 9; Length 487;

QY 652 aacaactgcacaacttcgaagaataatcgcgaagtcgagagatgattcttctgagc 711
 DB 363 AACAAATTGCATATTTGCAAGAAAGTACCGGCAATATATGGGTGAAGATTTATCAGGTT 422
 QY 712 tgaatcgaagaactgcagtcctcgagagaatcgaatcgaagaactgcagtcgagtcg 771
 DB 423 TGACAGGCAAAAGATTACAGGGTTTGAGAACACAGTTGGAATTCAGCCCTCTGCGTTC 482
 QY 772 ggcgaagaag 781
 DB 483 GTATGAAAAA 492

RESULT 14
 AM706936
 LOCUS 598 bp mRNA linear EST 03-DEC-2001
 DEFINITION sk08d08.y1 Gm-cl023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl023-3496 5' similar to TR:049351 049351 ANRI , MADS-BOX
 PROTEIN. ; mRNA sequence.
 AM706936
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 598)
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
 , A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 , Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 , R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 , R., Waterson, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com
 Insert length: 857 Std Error: 0.00
 High quality sequence stop: 422.
 Location/Qualifiers
 1. 598
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl023-3496"
 /clone_lib="Gm-cl023"
 /rlnsue_type="seed coats of greenhouse grown plants"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 cDNA library was constructed from mRNA isolated from seed
 coats (100-200mgs) of greenhouse grown plants. The
 library was prepared using the Life Technologies
 pSuperScript cDNA library construction kit. Complementary
 DNA was synthesized from mRNA using a poly (dt) sequence
 with a Not I restriction site. Sal I linkers adapters
 were ligated to the blunt-ended cDNA fragments followed by
 Not I digestion. The cDNA fragments were directionally
 cloned into the Not I-Sal I restriction site of the
 pSPORT1 vector. The ligated cDNA fragments were
 transformed into E.coli Electromax DH10B host cells. This
 library was constructed by Dr. Lila Vodkin and Dr. Anu
 Khanna."

BASE COUNT 189 a 117 c 138 g 153 t 1 others

ORIGIN
 Query Match 16.7%; Score 213.6; DB 9; Length 598;
 Best Local Similarity 65.9%; Pred. No. 2.4e-25;
 Matches 309; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 359 gatggggggggaagaacgctgacgcgagatcgaataactcgcagcgccgagctgac 418
 DB 130 GATGGGGGAGAGTAAGATTGGATTGCAAGCATGACACCTCCACTGCGCTCAAGTGAC 189
 QY 419 ctctccacgcgcggaacggagatcctcgaagaagcgaagctcgcctcctcgcga 478
 DB 190 TTTCTCGAAGAGCAAGAAATGATTCCTTAACAAGCTAGAGAAATTTGCTTTGTGA 249
 QY 479 tgcggaagtcgagctcgtcattcctccagcaccgcgcgctcctacgactcgaac 538
 DB 250 TGCTGAAGTTGATTTGATTTGTTCTCCAGCAGCTGCAAGCTTTATGACTATGCAAGTAC 309
 QY 539 cagcatgaatcagttatagatcgtgacgcgcaagcccaagaagaagcagatcgtgc 598
 DB 310 AAGCATGAATCTGTGATTGTAACGCTACAACTAAAGAGGAAACCATCATCCTCAT 369
 QY 599 aaatcccaactcggagcttaagtttgcaagaaggagcagcagcttgagacaact 658
 DB 370 GAATCCGGCTTCACAGCGAAGTTTGGCAGACAGAACGCAAGCTTGAGGCAACAGCT 429
 QY 659 gcacaactgcagaagaataatcgcgaagtcgagcggagatcctctgagctgaatgt 718
 DB 430 TCAGTACTTGCAGGAATGCCACAGCAATTAATGGGGGAGAACTTATGCTTTGGGTAT 489
 QY 719 caaagaactgcagtcctcgagagaatcgaatcgaagaagcctcggtggtcgcaaa 778
 DB 490 TAAAGAACTACAAAGCTGTGAAAACCACTGGAGATGAGTTAAAGGCTGTCGCGATGAT 549
 QY 779 gaagaccatccttgatagatgagatcagatcgaattgaatcaagaagca 827
 DB 550 AAATGACCACGATTGTACTATGATGATGCAAGAACTACGCTTAATGCA 598

RESULT 15
 BE445262
 LOCUS 587 bp mRNA linear EST 25-JUL-2000
 DEFINITION WHE1133_A05_A09Zs Wheat etiolated seedling root normalized cDNA
 library Trilicium aestivum cDNA clone WHE1133_A05_A09, mRNA
 sequence.
 BE445262
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Trilicium aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triliceae; Trilicium.
 1 (bases 1 to 587)
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 , P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
 Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105959773
 Fax: 5105959818
 Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: StrataGene SK primer.
 Location/Qualifiers
 1. 587

FEATURES
 source

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 08:38:25 ; Search time 24.9 Seconds
(Without alignments)
235,427 Million cell updates/sec

Title: US-09-970-624-2
Perfect score: 1216
Sequence: 1 MGRGKIVIRINDSTRQVY.....POONIEPSTAKLGLQLIP 240

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCNUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	426.5	35.1	252	1	US-08-460-512-5
2	426.5	35.1	285	1	US-08-460-512-2
3	418.5	34.4	252	1	US-08-460-512-4
4	417	34.3	246	4	US-09-067-800-8
5	417	34.3	246	4	US-09-349-677-8
6	409.5	33.7	248	1	US-08-460-512-7
7	405	33.3	248	4	US-09-067-800-6
8	405	33.3	248	4	US-09-349-677-6
9	401	33.0	248	2	US-08-867-087B-17
10	393	32.3	253	3	US-08-592-214A-4
11	393	32.3	253	3	US-08-659-188-4
12	393	32.3	253	3	US-08-655-227-4
13	393	32.3	253	3	US-08-655-241-4
14	393	32.3	253	3	US-09-149-976-4
15	393	32.3	253	3	US-09-398-326-4
16	390.5	32.1	242	4	US-09-067-800-2
17	390.5	32.1	242	4	US-09-067-800-2
18	390.5	32.1	242	4	US-09-105-652-2
19	388	31.9	255	2	US-08-592-214A-6
20	388	31.9	255	2	US-08-659-188-6
21	388	31.9	255	3	US-08-655-227-6
22	388	31.9	255	3	US-08-655-241-6
23	388	31.9	255	4	US-09-149-976-6
24	388	31.9	255	4	US-09-398-326-6
25	385	31.7	273	2	US-08-592-214A-8
26	385	31.7	273	2	US-08-659-188-8
27	385	31.7	273	3	US-08-655-227-8

28	385	31.7	273	3	US-08-655-241-8	Sequence 8, Appli
29	385	31.7	273	4	US-09-149-976-8	Sequence 8, Appli
30	385	31.7	273	4	US-09-398-326-8	Sequence 8, Appli
31	383.5	31.5	225	2	US-08-867-087B-55	Sequence 55, Appli
32	383.5	31.5	255	2	US-08-576-156-2	Sequence 2, Appli
33	383.5	31.5	300	2	US-08-592-214A-2	Sequence 2, Appli
34	383.5	31.5	300	3	US-09-149-976-2	Sequence 2, Appli
35	383	31.5	256	3	US-08-659-188-2	Sequence 2, Appli
36	383	31.5	256	3	US-08-655-227-2	Sequence 2, Appli
37	383	31.5	256	3	US-08-655-241-2	Sequence 2, Appli
38	383	31.5	256	4	US-09-398-326-2	Sequence 2, Appli
39	382.5	31.5	255	2	US-08-592-214A-10	Sequence 10, Appli
40	382.5	31.5	255	3	US-08-659-188-10	Sequence 10, Appli
41	382.5	31.5	255	3	US-08-655-227-10	Sequence 10, Appli
42	382.5	31.5	255	3	US-08-655-241-10	Sequence 10, Appli
43	382.5	31.5	255	3	US-09-149-976-10	Sequence 10, Appli
44	382.5	31.5	255	4	US-09-398-326-10	Sequence 10, Appli
45	381	31.3	257	2	US-08-867-087B-2	Sequence 2, Appli

ALIGNMENTS

```

RESULT 1
US-08-460-512-5
; Sequence 5, Application US/08460512
; Patent No. 5744693
GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFSKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Treccartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,512
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-512-5
Query Match 35.1%; Score 426.5; DB 1; Length 252;
Best Local Similarity 41.1%; Pred. No. 6.6e-33;

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Matches 102; Conservative 49; Mismatches 74; Indels 23; Gaps 7;

QY 2 GRGKIVIRIDNSTSRQVTFKRRNGIFPKAKELAILCDAEVGLVFSSTGRLYESSSTS 61
Db 18 GRGKIEIKRIENTNTNQVTFCKRRNGILLKAVELSVLCDAEVALVFSRRGLYEYSNNS 77
QY 62 MKSVIDRYGKAKEEQ---VYANPNSELKFWOREASLROOLHNLQENTROLTGDDLSGL 118
Db 78 VKGIERKKAISDNTSGVAELINAQ--YYOESAKLRQOITISONSNRQLMGETIGSM 135
QY 119 NVELOSLENOLETSRGVRAKKDHLIDELIDLNKASLPHQENTDLYNKINLIREND 178
Db 136 SPEKLENLGRLESTTRIRSKKNELLFSEIDYMKREVDLHNDQILRAKI----AENE 191
QY 179 ELHKIYETEGPSGVNRESPTPFNFAYETRDVPVQ---LELSTLPQONNIEPSTA--- 231
Db 192 RNPSSISLMPGSGNVFQALMPPP-----QTOSQPFDSRNVFYQVAL-QPNNHYSAGRQ 244
QY 232 PKIGLOLI 239
Db 245 DQTAQLV 252

RESULT 2

US-08-460-512-2
; Sequence 2, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFSKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,512
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-512-2

Query Match 35.1%; Score 426.5; DB 1; Length 285;
Best Local Similarity 41.1%; Pred. No. 7,9e-33;
Matches 102; Conservative 49; Mismatches 74; Indels 23; Gaps 7;

QY 2 GRGKIVIRIDNSTSRQVTFKRRNGIFPKAKELAILCDAEVGLVFSSTGRLYESSSTS 61
Db 51 GRGKIEIKRIENTNTNQVTFCKRRNGILLKAVELSVLCDAEVALVFSRRGLYEYSNNS 110
QY 62 MKSVIDRYGKAKEEQ---VYANPNSELKFWOREASLROOLHNLQENTROLTGDDLSGL 118
Db 111 VKGIERKKAISDNTSGVAELINAQ--YYOESAKLRQOITISONSNRQLMGETIGSM 168
QY 119 NVELOSLENOLETSRGVRAKKDHLIDELIDLNKASLPHQENTDLYNKINLIREND 178
Db 169 SPEKLENLGRLESTTRIRSKKNELLFSEIDYMKREVDLHNDQILRAKI----AENE 224
QY 179 ELHKIYETEGPSGVNRESPTPFNFAYETRDVPVQ---LELSTLPQONNIEPSTA--- 231
Db 225 RNPSSISLMPGSGNVFQALMPPP-----QTOSQPFDSRNVFYQVAL-QPNNHYSAGRQ 277
QY 232 PKIGLOLI 239
Db 278 DQTAQLV 285

RESULT 3

US-08-460-512-4
; Sequence 4, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFSKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,512
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-512-4

Query Match 34.4%; Score 418.5; DB 1; Length 252;
Best Local Similarity 40.0%; Pred. No. 3,8e-32;
Matches 104; Conservative 46; Mismatches 63; Indels 47; Gaps 9;

OY 2 GKGIVIRINDNSTROYTFKRRNGIFKRAKELALICDAEVGLVIFSSGTGLYEYSTS 61
 DB 18 GKGKIEIRIENTINROYTFCKRRNGLLKKAVELSVLCDAEVALVIFSSRGLYEYSSNS 77
 OY 62 MGSVIDRYGKAKKEQO---VVA NPSELKFWOREASLRQOLJHNLQENYROLTGDDLSGL 118
 DB 78 VKGTIERPKKAISDMSNTGSAVEINAO---YYQESAKLRQOIIISIONSRLQMETIGSM 135
 OY 119 NVKELQSLLENQLETSLRGVRAKKDHLLIDETHDLNRKASLPHQENTDLYNKINLIRQEND 178
 DB 136 SPKELRLNEGRILDRSVNRKSKNELLPFAELIDYMOKR-----EVDLHN-----DNO 181
 OY 179 ELHKIYETEG-----PSGVNRE-----SPRPFNAVETRDVPVQLELSTLPQ 222
 DB 182 LIRAKIAENERNRNPMSLMPGSGNTEQIMPPQTOPQPF-----DSRNYFOVAL-Q 232
 OY 223 QNNIEPSTA---PKLGLQLI 239
 DB 233 PNNHHYSSAGREDJVALQLV 252

RESULT 4

US-09-067-800-8
 ; Sequence 8, Application US/09067800
 ; Patent No. 6198024
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Ferrandiz, Cristina
 ; TITLE OF INVENTION: Seed Plants Characterized by Delayed
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/067, 800
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-UD 2948
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 246 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-067-800-8

Query Match 34.3%; Score 417; DB 4; Length 246;

Best Local Similarity 38.7%; Pred. No. 5,1e-32;

Matches 96; Conservative 53; Mismatches 73; Indels 26; Gaps 7;

OY 1 MGRGKIVIRINDNSTROYTFKRRNGIFKRAKELALICDAEVGLVIFSSGTGLYEYSS 60
 DB 16 IGRGKIEIRIENTINROYTFCKRRNGLLKKAVELSVLCDAEVALVIFSTRGRLEYEVANN 75
 OY 61 SMKSVIDRYGKAKKEQO---VVA NPSELKFWOREASLRQOLJHNLQENYROLTGDDLS 116
 DB 117 GIVNKELOSLLENQLETSLRGVRAKKDHLLIDETHDLNRKASLPHQENTDLYNKI---NL 172

DB 76 SVRGTIERYKAKCSD---AVNPPTITEANTQYQOESAKLRQIRIDIONLNRHILLESIG 132
 OY 117 GIVNKELOSLLENQLETSLRGVRAKKDHLLIDETHDLNRKASLPHQENTDLYNKI---NL 172
 DB 133 SLNFKELKNIESRLKIEKISVRSKKHMLVALEYOKRETELQNDNMYLRSKITERTGL 192
 OY 173 IROENDLHK-KIYETEGPSGVNRESPTPNNFAVETRDVPVQLELSTLPQOQNNIEPSTA 231
 DB 193 QOQESSVIHQGYYES-GVYSSHQSGYNNNTAVNVLE-----PNQSSNQDQP 241
 OY 232 PKLGLQLI 239
 DB 242 P---LQLV 246

RESULT 5

US-09-349-677-8
 ; Sequence 8, Application US/09349677
 ; Patent No. 6288305
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Ferrandiz, Cristina
 ; TITLE OF INVENTION: Seed Plants Characterized by Delayed
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/349,677
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/067,800
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-UD 2948
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 246 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-349-677-8

Query Match 34.3%; Score 417; DB 4; Length 246;

Best Local Similarity 38.7%; Pred. No. 5,1e-32;

Matches 96; Conservative 53; Mismatches 73; Indels 26; Gaps 7;

OY 1 MGRGKIVIRINDNSTROYTFKRRNGIFKRAKELALICDAEVGLVIFSSGTGLYEYSS 60
 DB 16 IGRGKIEIRIENTINROYTFCKRRNGLLKKAVELSVLCDAEVALVIFSTRGRLEYEVANN 75
 OY 61 SMKSVIDRYGKAKKEQO---VVA NPSELKFWOREASLRQOLJHNLQENYROLTGDDLS 116
 DB 76 SVRGTIERYKAKCSD---AVNPPTITEANTQYQOESAKLRQIRIDIONLNRHILLESIG 132
 OY 117 GIVNKELOSLLENQLETSLRGVRAKKDHLLIDETHDLNRKASLPHQENTDLYNKI---NL 172

RESULT 8
US-09-349-677-6

; Sequence 6, Application US/09349677

; Patent No. 6288305

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; APPLICANT: Ferrandiz, Cristina

; TITLE OF INVENTION: Seed Plants Characterized by Delayed

; TITLE OF INVENTION: Seed Dispersal

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/349,677

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/067,800

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-UD 2948

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 248 amino acids

; TYPE: amino acid

; TOPOLOGY: Linear

; MOLECULE TYPE: protein

; US-09-349-677-6

Query Match 33.3%; Score 405; DB 4; Length 248;

Best Local Similarity 43.98; Pred. No. 7.2e-31;

Matches 90; Conservative 42; Mismatches 55; Indels 18; Gaps 5;

QY 1 MGRGKIVIRIDNSTSRQVTFESKRRNGIFKKAKELAIICDAEVLIVFSSGTGRLEYEST 60
 DB 16 IGRGKIEIKRIENTNRQVTFCKRRNGILKKAYELSVLCDAEVALVIFSTGRLEYEANN 75
 QY 61 SMKSVIDRYGAKKEQOVVAMPNS---ELKFWQREASLSRQQLHNIQENYRQLTGDDLS 116
 DB 76 SVRGTEIERYKKACSD---AVNPSPYTEANTQYQOEASKLRQIRIDIONSRRHIVGESLG 132
 QY 117 GINVELOSLENOLETSLRGVRAKDDHLIDEIHDINKKASLFHOENTDLYNKI----- 170
 DB 133 SLNKEELKNEGRLEKGIKSVYRSKKNELVAIEYWMOKREKELQNNNYLFAKIAEGARL 192
 QY 171 NLIRQENDELH-KRIYETEGPSGVN 194
 DB 193 NPDOESSVIGTITYE---SGVS 213

RESULT 9

US-08-867-087B-17

; Sequence 17, Application US/08867087B

; Patent No. 5990386

; GENERAL INFORMATION:

; APPLICANT: An, Gynheung

; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell Leigh &

; STREET: One World Trade Center

; STREET: 121 S.W. Salmon Street

; STREET: Suite 1600

; CITY: Portland

; STATE: Oregon

; COUNTRY: United States of America

; ZIP: 97204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: disk, 3-1/2 inch

; OPERATING SYSTEM: MS DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/867,087B

; FILING DATE: June 2, 1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/323,449

; FILING DATE: October 14, 1994

; APPLICATION NUMBER: U.S. 08/485,981

; FILING DATE: June 7, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Alan. E.

; REGISTRATION NUMBER: 35,123

; REFERENCE/DOCKET NUMBER: 4630-47071

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 248 amino acid residues

; TYPE: amino acid

; TOPOLOGY: Linear

; US-08-867-087B-17

Query Match 33.0%; Score 401; DB 2; Length 248;

Best Local Similarity 37.0%; Pred. No. 1.7e-30;

Matches 94; Conservative 50; Mismatches 74; Indels 36; Gaps 7;

QY 1 MGRGKIVIRIDNSTSRQVTFESKRRNGIFKKAKELAIICDAEVLIVFSSGTGRLEYEST 59
 DB 1 IGRGKIEIKRIENTNRQVTFCKRRNGILKKAYELSVLCDAEVALVIFSTGRLEYEANN 60
 QY 60 TMSKSVIDRYGK-----AKEEQOVVAMPNSLEKFWQREASLSRQQLHNIQENYR 108
 DB 61 QSMRTILERYOKFSYGGPDTAIONKENELVQSSRNEYLK-----LQARVENLQRTOR 112
 QY 109 QLTGDDLSGINVELOSLENOLETSLRGVRAKDDHLIDEIHDINKKASLFHOENTDLYN 168
 DB 113 NLGEDLGITGIELBEQLEKQDSLSRHRIRSTQHMLOLDLQORREOMLCEANKCLRR 172
 QY 169 KINLIRQENDELHAKKI-----YETEGPSGVNRESPTFEN--FAYVETRDVYQDEL 217
 DB 173 KL-----EESNQLHGQVMEHATLLGYEROSPRAVQOVPPHGGNGFPHSLDAEAAPT- 227
 QY 218 STLPOONNIEPSTA 231
 DB 228 GTFPEOMNNSCVTA 241

RESULT 10

US-08-592-214A-4

; Sequence 4, Application US/08592214A

; Patent No. 5811536

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

```

; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-592-214A-4

```

```

Query Match          32.3%; Score 393; DB 2; Length 253;
Best Local Similarity 35.6%; Pred. No. 1e-29;
Matches 83; Conservative 56; Mismatches 62; Indels 32; Gaps 5;

```

```

QY 1 MGRKIVIRIDNSTSRQVTFKRRNGIFKKAKELATLDCDAEVLVFSRGRLEYEST 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRGVQLRKLEKINROVTFKRRRAGLKKAKHETSVLDCDAEVALVFSHKGLFEYSTD 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 S-MKSVIDRYGK-AKEEQOVANPNSELKFWOREAASLRQOLHNLQENYRLTGDDLSGL 118
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SCMEKILERYERYSAERQLAPESDSNTNMSMEYNRLKAKTELLERNQRYLGEDLQAM 120
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 NKELOSLLENQLETSIRGVRAKDHLLIDETIDLNKKSALFHQENTDLYNKI----NLIR 174
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SPKELONLQOOLDTALKHTRSRKNQLMYDSINELQREKAKLOEQNSMLSKQIKERENVLR 180
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 QENDELHKRIYETEGSPGVNRESPTPFNFVAVETRDVPVQLSTLTPPOONNIE 227
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 AAOEQWDEQNH-----GHNMPPPP-----PQOHQIQ 207

```

```

RESULT 11
US-08-659-188-4
; Sequence 4, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
;
; 9

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-659-188-4

```

```

Query Match          32.3%; Score 393; DB 3; Length 253;
Best Local Similarity 35.6%; Pred. No. 1e-29;
Matches 83; Conservative 56; Mismatches 62; Indels 32; Gaps 5;

```

```

QY 1 MGRKIVIRIDNSTSRQVTFKRRNGIFKKAKELATLDCDAEVLVFSRGRLEYEST 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRGVQLRKLEKINROVTFKRRRAGLKKAKHETSVLDCDAEVALVFSHKGLFEYSTD 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 S-MKSVIDRYGK-AKEEQOVANPNSELKFWOREAASLRQOLHNLQENYRLTGDDLSGL 118
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SCMEKILERYERYSAERQLAPESDSNTNMSMEYNRLKAKTELLERNQRYLGEDLQAM 120
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 NKELOSLLENQLETSIRGVRAKDHLLIDETIDLNKKSALFHQENTDLYNKI----NLIR 174
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SPKELONLQOOLDTALKHTRSRKNQLMYDSINELQREKAKLOEQNSMLSKQIKERENVLR 180
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 QENDELHKRIYETEGSPGVNRESPTPFNFVAVETRDVPVQLSTLTPPOONNIE 227
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 AAOEQWDEQNH-----GHNMPPPP-----PQOHQIQ 207

```

```

RESULT 12
US-08-655-227-4
; Sequence 4, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

```



```

Db      1  MGRGRVQLKRIENKINQVTFKRRAGLMMKKAHEISVLCDAEVALVPSHKGILFEYSTD 60
QY      61  S-MKSVIDRYGK-AKEEOVVANPNSELKFWOREASLRQOLHNIQENYROLTGDDLSGL 118
Db      61  SCMEKILEYERYSYAERQLAPESDSNTNMSMEYNRKLAKIELERNQRYHLEGDLQAM 120
QY      119 NKEIQLSLENOLETSLRGVRAKDHLLIDEIHDLNKKASLPHOENTDLYNKI---NLIR 174
Db      121 SPKELQNLQEQOLDTALKHTRSKKNQMLYDSINELQREKAIQONSMLSKOIKERENVLR 180
QY      175 QENDELHKKIYETEGSPGVNRESPPPENFAVETRDVPVQLELSTLPQONNIE 227
Db      181 AOEQOWDEQNH-----GHNMPPPP-----POOHIO 207

```

RESULT 15
US-09-398-326-4
; Sequence 4, Application US/09398326
; Patent No. 6355863

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF SEQUENCES: 26
REPRODUCTIVE Development and Methods of Making Same

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California

COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-398-326-4

Query Match 32.38; Score 393; DB 4; Length 253;
Best Local Similarity 35.68; Pred. No. 1e-29;
Matches 83; Conservative 56; Mismatches 62; Indels 32; Gaps 5;

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QY      1  MGRKIVIRRIDNSTSRVTFKRRNGIFPKAKELATICDAEGLVTFSSGRLEYEYST 60
Db      1  MGRGRVQLKRIENKINQVTFKRRAGLMMKKAHEISVLCDAEVALVPSHKGILFEYSTD 60
QY      61  S-MKSVIDRYGK-AKEEOVVANPNSELKFWOREASLRQOLHNIQENYROLTGDDLSGL 118
Db      61  SCMEKILEYERYSYAERQLAPESDSNTNMSMEYNRKLAKIELERNQRYHLEGDLQAM 120
QY      119 NKEIQLSLENOLETSLRGVRAKDHLLIDEIHDLNKKASLPHOENTDLYNKI---NLIR 174

```

```

Db      121 SPKELQNLQEQOLDTALKHTRSKKNQMLYDSINELQREKAIQONSMLSKOIKERENVLR 180
QY      175 QENDELHKKIYETEGSPGVNRESPPPENFAVETRDVPVQLELSTLPQONNIE 227
Db      181 AOEQOWDEQNH-----GHNMPPPP-----POOHIO 207

```

Search completed: August 11, 2002, 09:36:43
Job time: 3498 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2002, 08:42:20 ; Search time 43.45 Seconds

(without alignments)
530.758 Million cell updates/sec

Title: US-09-970-624-2

Perfect score: 1216
Sequence: 1 MGRKIVIRIDNSTSRQVT.....PQNNIEPSTAPKLGILIP 240

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	729.5	60.0	234	2	T17029
2	666	54.8	228	2	T05621
3	643.5	52.9	227	2	H84614
4	638.5	52.5	234	2	T52100
5	636.5	52.3	234	2	A84515
6	605	49.8	240	2	T09700
7	589	48.4	239	2	T45801
8	435	35.8	261	2	S51935
9	428.5	35.2	222	2	S51934
10	426.5	35.1	284	2	T05033
11	426.5	35.1	284	2	A85214
12	425	35.0	261	2	T09603
13	420	34.5	262	2	T08039
14	419.5	34.5	230	2	T04000
15	418.5	34.4	252	2	A43484
16	417.5	34.3	242	2	J02212
17	417	34.3	246	2	E39534
18	416	34.2	229	2	T08040
19	414	34.0	258	2	G84858
20	409.5	33.7	248	2	T03592
21	408.5	33.6	248	2	T07185
22	405	33.3	248	2	A39534
23	405	33.3	254	2	T10185
24	403	33.1	265	2	T02261
25	402.5	33.1	236	2	S59480
26	402.5	33.1	242	2	T10486
27	402.5	33.1	242	2	T09571
28	401	33.0	248	2	T04170
29	401	33.0	257	2	S53306

30	401	33.0	259	2	T01700	hypothetical prote
31	399.5	32.9	248	2	S20886	MADS box protein s
32	394.5	32.4	250	2	T04167	MADS box protein s
33	393	32.3	246	2	T17023	MADS box protein 1
34	392	32.2	286	2	J02289	floral homeotic pr
35	391.5	32.2	239	2	A44343	promotes sex organ
36	390.5	32.1	242	2	S71208	MADS box protein A
37	390	32.1	247	2	S60307	fbp6 protein - gar
38	386.5	31.8	227	2	S23730	MADS box protein T
39	385.5	31.7	254	2	S52236	MADS box protein a
40	385	31.7	253	2	S57586	MADS-box regulator
41	385	31.7	273	2	T03410	MADS box protein h
42	384	31.6	250	2	T07100	MADS box protein h
43	383.5	31.5	225	2	T04168	MADS box protein A
44	383	31.5	256	2	S27109	MADS box protein A
45	381.5	31.4	219	2	S46526	MADS box protein m

ALIGNMENTS

RESULT 1

T17029
MADS-box transcription factor DEFH125 - garden snapdragon

C:Species: Antirrhinum majus (garden snapdragon)

C>Date: 15-Oct-1999 #sequence #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T17029

R:Zachgo, S.; Saedler, H.; Schwarz-Sommer, Z.

Plant J. 11, 1043-50, 1997

A:Title: Pollen-specific expression of DEFH125, a MADS-box transcription factor in An

A:Reference number: Z14458; MUID:9193074

A:Accession: T17029

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-234 <ZAC>

A:Cross-references: EMBL:Y10750

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho

C:Keywords: transcription factor

Query Match	60.0%	Score 729.5;	DB 2;	Length 234;
Best Local Similarity	63.2%	Pred. NO. 1.5e-42;		
Matches 146;	Conservative 32;	Mismatches 52;	Indels 1;	Gaps 1;
QY	1	MGRKIVIRIDNSTSRQVTFSKRRNGIFKKAKELATLCOAEVGLVFSSTGRLEYSSST 60		
DB	1	MGRKIVIRIDNSTSRQVTFSKRRNGIFKKAKELATLCOAEVGLVFSSTGRLEYSSST 60		
QY	61	SMKSVIDRYGKAKKEQGVANPNSEILKFWQREASLRQQLHNLQENYROLTGDDLSGLNV 120		
DB	61	SMKSVIDRYGKAKKEQGVANPNSEILKFWQREASLRQQLHNLQENYROLTGDDLSGLNV 120		
QY	121	KELOSLENQLETSKGVRAKRDHLIDEIHDNLNRKASLFHOENMDLKNKILNQENDEL 180		
DB	121	EDIHLEQLQLEMSLKGVCVRRKQVMMLTDEVHRLRRKGCHLHQENNELYEKVLDOENKEL 180		
QY	181	HKRIETEGSPGVNRESPTPENFAVETRDVYVLELSTLPQNNIEPSTA 231		
DB	181	CKKAGTQDVSAANGTALVPPGFAIGRQFPFIQLHLSQ-PEPENIETSTRA 230		
RESULT 2				
T05621				
MADS-box protein AG17 homolog F20D10.60 - Arabidopsis thaliana				
C:Species: Arabidopsis thaliana (mouse-ear cress)				
C>Date: 23-Apr-1999 #sequence #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999				
C:Accession: T05621				
R:Bayan, M.; Medler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer,				
submitted to the Protein Sequence Database, February 1999				
A:Reference number: Z15420				
A:Accession: T05621				
A:Molecule type: DNA				
A:Residues: 1-228 <BEV>				

Db 61 NIRSTIERKACSDSTNTSTVQELNA--AYYQESAKLRFQIQITQNSNRNLMDGLSS 118
QY 118 LNVKELQSLQENOLETSLGVRRAKDHLLIDETHLNKRKASLFHQENTDLYNKINLIRQEN 177
Db 119 LSVKELQOVENRLEKAIKIRSKHLLIVLEIENAKREIEMDNIYILRTKVAEVERYQ 178
QY 178 DELHKKIYETE 188
Db 179 OHNHQWVGSGE 189

RESULT 15

A43484
probable transcription factor BAG1 - rape
C:Species: Brassica napus (rape)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: A43484
R:Mandel, M.A.; Bowman, J.L.; Kempin, S.A.; Ma, H.; Meyerowitz, E.M.; Yanofsky, M.F.
Cell 71, 133-143, 1992
A:Title: Manipulation of flower structure in transgenic tobacco.
A:Reference number: A43484; MUID:93008236
A:Accession: A43484
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-252 <MAN>
A:Cross-references: GB:M99415; NID:g167125; PIDN:AAA32985.1; PID:g167126
A>Note: sequence extracted from NCBI backbone (NCBI:115468)
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription regulation
F:18-73/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 34.4%; Score 418.5; DB 2; Length 252;
Best Local Similarity 40.0%; Pred. No. 2e-21;
Matches 104; Conservative 46; Mismatches 63; Indels 47; Gaps 9;
QY 2 GRGKIVIRIDNSTSRQYTFKRRNGIFKAKELAILCDAEVGLVTFSSGTGRIEYSSTS 61
Db 18 GRGKIEIKRIENTTNRQYTFKRRNGILKAYELSLCDAEVALIVFSSRGRIEYSNNS 77
QY 62 MKSVIDRIGKAKEEQ---VANPNSLKFQWREASLRQOLHNLQENYROLTGDDLSGL 118
Db 78 VGLTIERKKAISDNSNTGVAEINAQ--YYQESAKLRQOIISIONSROLMGFTIGSM 135
QY 119 NVKEIQLQENOLETSLGVRRAKDHLLIDETHLNKRKASLFHQENTDLYNKINLIRQEND 178
Db 136 SPEKLNLEGRIDRSVNNIRSKNELLEAFIDYMQK-----EVDLHN-----DNQ 181
QY 179 ELHKKIYETEG-----PSGVNRE-----SPFPNFAYVETRDVPVQLELSTLPQ 222
Db 182 LLRAKIAEENRNNPMSLMPGCSNVEQIMPPQTPQPF-----DSRNVFOVAAL-Q 232
QY 223 ONNIEPSTA---PKLGLOLI 239
Db 233 PNNHHYSSAGREDTALQIV 252

Search completed: August 11, 2002, 09:37:47
Job time: 3327 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 09:36:49 ; Search time 24.99 Seconds

(Without alignments)
371.856 Million cell updates/sec

Title: US-09-970-624-2

Perfect score: 1216
Sequence: 1 MGSKIVIRINDNSTROYT.....POONIEPSTARKLGILIP 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666	54.8	228	1	AG1Y_ARATH
2	643.5	52.9	227	1	Q98406 arabidopsis
3	426.5	35.1	252	1	AG17_ARATH
4	419.5	34.5	230	1	AG18_ARATH
5	418.5	34.4	252	1	AG18_ARATH
6	417.5	34.3	246	1	AG18_ARATH
7	417	34.3	246	1	AG18_ARATH
8	414.5	34.1	242	1	AG18_ARATH
9	409.5	33.7	248	1	AG18_ARATH
10	408.5	33.6	248	1	AG18_ARATH
11	405	33.3	248	1	AG18_ARATH
12	390.5	32.1	242	1	AG18_ARATH
13	389.5	32.0	241	1	AG18_ARATH
14	386.5	31.8	227	1	AG18_ARATH
15	386	31.7	265	1	AG18_ARATH
16	385.5	31.7	254	1	AG18_ARATH
17	384	31.6	250	1	AG18_ARATH
18	383.5	31.5	255	1	AG18_ARATH
19	380	31.2	240	1	AG18_ARATH
20	378	31.1	250	1	AG18_ARATH
21	375	30.8	248	1	AG18_ARATH
22	373.5	30.7	252	1	AG18_ARATH
23	373	30.7	233	1	AG18_ARATH
24	372.5	30.6	268	1	AG18_ARATH
25	372	30.6	241	1	AG18_ARATH
26	365	30.0	250	1	AG18_ARATH
27	364.5	30.0	244	1	AG18_ARATH
28	363	29.9	214	1	AG18_ARATH
29	357	29.4	224	1	AG18_ARATH
30	354	29.1	219	1	AG18_ARATH
31	353.5	29.1	258	1	AG18_ARATH
32	353.5	29.1	251	1	AG18_ARATH
33	350.5	28.8	264	1	AG18_ARATH

34	349.5	28.7	254	1	AG19_SINAL
35	346.5	28.5	250	1	AG19_ARADE
36	337.5	27.8	209	1	GLOB_TOBAC
37	336.5	27.7	221	1	AG14_ARATH
38	335	27.5	210	1	FBP1_PETHY
39	307.5	25.3	39	1	GLOB_ANTMA
40	307	25.2	212	1	MAD2_PETHY
41	306	25.2	211	1	AG12_ARATH
42	303	24.9	231	1	MAD1_PETHY
43	297	24.4	214	1	CMB2_DIACA
44	296	24.3	196	1	FLC_ARATH
45	289.5	23.8	232	1	AP3_ARATH

ALIGNMENTS

RESULT 1	AG1Y_ARATH	STANDARD:	PRT:	228 AA.
AC	Q98206	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Agamous-like MADS box protein At4g37940.			
GN	At4g37940 OR F20D10.60.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_Taxid=3702;			
RM	[1]			
RP	SEQUENCE FROM N. A.			
RC	STRAIN=CV. COLUMBIA;			
RX	MEDLINE=20083488; PubMed=10617198;			
RA	Mayer K.F.X., Schueller C., Wambolt R., Murphy G., Volkhaert G.,			
RA	Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,			
RA	Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,			
RA	Weichselgartner M., de Simone V., Obermaier B., Macho R., Mueller M.,			
RA	Kreis M., Deiseny M., Puigdomenech P., Watson M., Schmidheini T.,			
RA	Reichert B., Portelle D., Perez-Alonso M., Boutry M., Bancroft I.,			
RA	Vos P., Hohelsel J., Zimmermann W., Wedler H., Riddle P.,			
RA	Langham S.-A., McCullagh B., Bilham L., Robben J.,			
RA	Van der Schueren J., Grymonprez B., Chang Y.-J., Vandebussche F.,			
RA	Breken M., Weljens I., Voet M., Bastiaens I., Aert R., Defoor E.,			
RA	Wetzellegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,			
RA	Holzer E., Brandt A., Peters S., van Stavelen M., Dirkse W.,			
RA	Moolijman P., Klein Lankhorst R., Rose M., Haut J., Koether P.,			
RA	Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,			
RA	De Keyser A., Buysschaert C., Gielen J., Villarroel R., De Clercq R.,			
RA	Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,			
RA	Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,			
RA	Petkov A., Rajendram M.A., Lyne M., Benes V., Reichmann S.,			
RA	Botkova D., Bloeker H., Scharte M., Grimm M., Loehner T.H.,			
RA	Gabel S., de Haan M., Maarse A.C., Schaefer M., Mueller Auer S.,			
RA	Dose C., Fuchs M., Fartmann B., Grandenath K., Dauner D., Herzel A.,			
RA	Neumann S., Argitgley A., Vitale D., Liqouri R., Piravandi E.,			
RA	Massenet O., Outgley F., Clabaud G., Mwendile A., Felber R.,			
RA	Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,			
RA	Cheldor F., Cooke R., Berger C., Monfort A., Cascuberta E.,			
RA	Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,			
RA	Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,			
RA	Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleske C.,			
RA	Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,			
RA	Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Hebermann K.,			
RA	Parnell L., Dedina N., Gnoj L., Schutz K., Huang E., Spiegel L.,			
RA	Sekon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,			
RA	Stokem T., Kalicki J., Graves T., Hamon G., Edwards J.,			
RA	Lafaille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,			
RA	Mior J., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,			
RA	Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,			
RA	Nelson J., Speth J., Ryan E., Andrews S., Geisel C., Layman D.,			
RA	Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,			

RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Malero A., Shah R.,
 RA Saby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lohi M., Johnson A.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:769-777(1999).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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 CC -----
 DR EMBL: AL035538; CAB37534.1; -;
 DR EMBL: AL161592; CAB80459.1; -;
 DR HSSP: P11831; ISRS.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 95 167 K-BOX.
 FT SEQUENCE 228 AA; 26411 MW; 87077BFB6CC4F7A6 CRC64;

Query Match 54.8%; Score 666; DB 1; Length 228;
 Best Local Similarity 59.0%; Pred. No. 2, 2e-37;
 Matches 138; Conservative 36; Mismatches 50; Indels 10; Gaps 3;

QY 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLIDAEVGLVIFSSGRLYEYSST 60
 DB 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLIDAEVGLVIFSSGRLYEYSST 60
 QY 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 DB 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 QY 121 KELQSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 DB 121 KELQSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 QY 121 NEUNSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 DB 121 NEUNSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 QY 181 HKKIVTEGSGVNRSPPTFPAVETRD-VVQLELSTLPQNNIEPSTAPK 233
 DB 181 HKKIVTEGSGVNRSPPTFPAVETRD-VVQLELSTLPQNNIEPSTAPK 233
 DB 181 YKRAYMANTNGFTHRE-----VAVADDESHQIROLIS---QPEHSDYDTPPR 225

RESULT 2
 AG17_ARATH STANDARD; PRT; 227 AA.
 AC Q3840; Q92050;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Agamous-like MADS box protein AG17.
 GN AG17 OR At2g22630 OR Y1922.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucoside II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLOMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Honning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE OF 8-227 FROM N.A.
 RC STRAIN=CV. LANDSBERG ERCTA; TISSUE=Root;
 RX MEDLINE=96004530; PubMed=7549482;
 RA Rounsley S.D., Ditta G.S., Yanofsky M.F.;
 RT "Diverse roles for MADS box genes in Arabidopsis development.";
 RL Plant Cell 7:1259-1269(1995).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: PREPARENTIALLY EXPRESSED IN ROOTS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -----
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 CC -----
 DR EMBL: AC006340; AAD15571.1; -;
 DR EMBL: U20186; AAC49084.1; -;
 DR HSSP: P11746; 1NMN.
 DR TRANSFAC: T03020; -;
 DR Mendel: 6456; Arabid; MADS; 6456.
 DR Mendel: 39770; Arabid; MADS; 39770.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 2.
 KM Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 95 167 K-BOX.
 FT DOMAIN 201 227 AVESSHAQVRLQSLQPEQSHYKTSNS -> QENPMHRLG
 FT SEQUENCE 227 AA; 26314 MW; 2C02283974D76594 CRC64;

Query Match 52.9%; Score 643.5; DB 1; Length 227;
 Best Local Similarity 57.0%; Pred. No. 6, 5e-36;
 Matches 131; Conservative 46; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLIDAEVGLVIFSSGRLYEYSST 60
 DB 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLIDAEVGLVIFSSGRLYEYSST 60
 QY 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 DB 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 QY 121 KELQSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 DB 121 KELQSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 QY 121 NEUNSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 DB 121 NEUNSLNQLSTLKGVRKKDHLIDELHDLNRKASLFEQENTDLYNKINLRQENDEL 180
 QY 181 HKKIVTEGSGVNRSPPTFPAVETRD-VVQLELSTLPQNNIEPSTAPK 233
 DB 181 HKKIVTEGSGVNRSPPTFPAVETRD-VVQLELSTLPQNNIEPSTAPK 233
 DB 181 YKRAYMANTNGFTHRE-----VAVADDESHQIROLIS---QPEHSDYDTPPR 225

Db 121 KELLONISQLEMSLRGIRMRQELTNEIKELTRKRLVHHEMLSRKQRIHOENVEL 180
 Oy 181 HKKIYEEGSGVNRSPFPNFVETRPVQLEISTIPQOONIEPT 230
 Db 181 YKRAYGNTNGLGHLEVD--AYVESH-AQVRLQLSQ-PEOSHVKTS 225

RESULT 3
 AG_ATH ID AG_ATH STANDARD; PRT; 252 AA.

AC P17839;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE AGAMOUS protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

SEQUENCE FROM N.A.
 RP STRAIN-CV. LANDSBERG ERECTA;
 RX MEDLINE=9030968; PubMed=1973265;
 RA Yanofsky M.F., Ma H., Bowman J.L., Drews G., Feldmann K.A.,
 RA Meyerowitz E.M.;
 RT "The protein encoded by the Arabidopsis homeotic gene agamous
 RT resembles transcription factors.";
 RL Nature 346:35-39(1990).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS.

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: MUTATIONS IN THE AG GENE RESULT IN THE REPLACEMENT
 CC OF THE SIX STAMENS BY SIX PETALS AND OF THE CARPELS BY A NEW
 CC FLOWER.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).

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DR EMBL: X53579; CAA37642.1; ALT_INT.
 DR PIR: S10933; S10933.
 DR HSSP: P11746; INNM.
 DR TRANSFAC: T01007;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF00319; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DOMAIN 19 73 MADS.
 FT DOMAIN 112 184 K-BOX.
 FT CONFLICT 1 1 M->T (IN REF. 1).
 SQ SEQUENCE 252 AA; 28723 MW; 4E7591AD85654C1C CRC64;

Query Match 35.18; Score 426.5; DB 1; Length 252;
 Best Local Similarity 41.18; Pred. No. 1,4e-21;
 Matches 102; Conservative 49; Mismatches 74; Indels 23; Gaps 7;

Oy 2 GREKIVIRIDNSTSPQFFSRKRNQIFKAKELAILDDEAGLVIFSTGRLEYST 61
 Db 18 GCKIKIRKLENTNTNQVFCRRNGLKKAELSLVCDAEVALLVFSRGLYEYSNN 77
 Oy 62 MMSVIDRYKAKEEEO---VANPSELKFWQREASLRLQDLNQLQENTROLTGDSL 118
 Db 78 VKGTIERKKKALSDNSNTGNSVAEINQ--YQOESKAKLQOITISIONSROLMGETISM 135
 Oy 119 NVKELQSLNQLTSLRGVRAKDHLLIDEINDLRKASLFEQEMNDLYNKINLROEND 178
 Db 136 SPKELNLGRLERSTIRSKNELFSELDYMQREYDLNDQILAKT----AENE 191
 Oy 179 ELKKIYETEGSGVNRSPFPNFVETRPVQ---LEISTIPQOONIEPTA--- 231
 Db 192 RNNPSTSLMPGGSNYQLMPP-----QTOSQPTDSRYFQVAL-QPNNHYSAGNQ 244

RESULT 4
 AG_ATH ID AG_ATH STANDARD; PRT; 230 AA.

AC 038836;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Agamous-like MADS box protein AG11.
 GN AG11 OR AT4G09960 OR T5L19.90.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

SEQUENCE FROM N.A.
 RP STRAIN-CV. LANDSBERG ERECTA; TISSUE=flower;
 RX MEDLINE=96004530; PubMed=7549482;
 RA Rounsley S.D., Ditta G.S., Yanofsky M.F.;
 RT Diverse roles for MADS box genes in Arabidopsis development.";
 RL Plant Cell 7:1259-1269(1995).

RP SEQUENCE FROM N.A.
 RP STRAIN-CV. COLUMBIA;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wandut R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Oberwälder P., Macho R., Mueller M.,
 RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnel U., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Billam L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzengrter T., Bothé G., Ramsperger U., Hilbert H., Bruun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirse W.,
 RA Woolfman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA de Keyser A., Buyschaert C., Gielen A., Villartiel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,
 RA Pettelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe K., Grimm M., Loehmet T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Faltmann B., Grandeth K., Dauner D., Herzl A.,
 RA Neumann S., Argitlou A., Vitale D., Iqbal G., Piravandi E.,
 RA Messenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lechanny A., Aubourg S.,
 RA Cheifor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,

RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances S., Stocker S.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kallio J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Clout J., Abbott A., Scott K., Johnson D.,
 RA Mox P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., All J., Bergdorf A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
 RA Swaby I.R., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Rodriguez M., Hoffman J., Till S.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:769-777(1999).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.

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CC -----
 DR EMBL: U20182; AAC49080.1; -;
 DR EMBL: AL049481; CAB39620.1; -;
 DR EMBL: AL161516; CAB78119.1; -;
 DR HSSP: P11746; 1NMN.
 DR TRANSFAC: T03009; -;
 DR Mendel: 6452; Arabid; MADS; 6452.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 96 168 K-BOX.
 SQ SEQUENCE 230 AA; 26183 MW; 336C383355E6CB51 CRC64;

Query Match 34.5%; Score 419.5; DB 1; Length 230;
 Best Local Similarity 45.0%; Pred. No. 3.5e-21;
 Matches 86; Conservative 42; Mismatches 58; Indels 5; Gaps 2;

QY 1 MGKGIKIRIRIDNSTRGVTFKRRNGIFKKAKELALICDAEGLVIFSSGRLEYESTS 60
 DB 1 MGKGIKIRIRIDNSTRGVTFKRRNGIFKKAKELALICDAEGLVIFSSGRLEYESTS 60
 QY 61 SMSKVIDRYKAKEEQ--OVANPNSELKFWQREASLRQQLHNIQENYROLTGDDLSG 117
 DB 61 NISITLERYKAKCSDTNTSTVOEINA--AYQOESAKLRQOQIOTIONSNRNMGDSLS 118
 QY 118 LNKELQSLQENQLETSIRGVAKRKDHLLIDEIDHNRKASLPHQENTDLYNKINLRQEN 177
 DB 119 LSKVELKQVNRLEKAKISIRSKKHELLWEIENAKRTEIDNENIYLRKVAEVERQ 178
 QY 178 DELHKIYETE 188
 DB 179 QHHHGVSGSE 189

RESULT 5
 AG-BRANA STANDARD; PRT; 252 AA.
 ID AG-BRANA
 AC Q01540;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE AGAMOUS protein.
 GN Agl.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WESTAR;
 RX MEDLINE=93008236; PubMed=1356631;
 RA Mandel M.A., Bowman J.L., Kempln S.A., Ma H., Meyerowitz E.M.,
 RA Yanofsky M.F.;
 RL Cell 71:133-143(1992).
 RT "Manipulation of flower structure in transgenic tobacco."
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRP-TYPE TRANSCRIPTION FACTORS (K-BOX).

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CC -----
 DR EMBL: M99415; AAA32985.1; -;
 DR PIR: A43484; A43484.
 DR HSSP: P11746; 1NMN.
 DR TRANSFAC: T01773; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DOMAIN 19 73 MADS.
 FT DOMAIN 112 184 K-BOX.
 SQ SEQUENCE 252 AA; 28778 MW; 7C1EF7C96C19EACE CRC64;

Query Match 34.4%; Score 418.5; DB 1; Length 252;
 Best Local Similarity 40.0%; Pred. No. 4.5e-21;
 Matches 104; Conservative 46; Mismatches 63; Indels 47; Gaps 9;

QY 2 MGKGIKIRIRIDNSTRGVTFKRRNGIFKKAKELALICDAEGLVIFSSGRLEYESTS 61
 DB 18 GKGKIEIKRIETNTTRQVTFKRRNGILKAKVELSVLCDAEVALIVSSRRRLKLEYENNS 77
 QY 62 MGSVIDRYKAKEEQ--OVANPNSELKFWQREASLRQQLHNIQENYROLTGDDLSG 118
 DB 78 VSGTIERYKKAISDSNNSGVAEINAO--YYQOESAKLRQOQIOTIONSNRNMGDSLS 135
 QY 119 NKELOSLQENQLETSIRGVAKRKDHLLIDEIDHNRKASLPHQENTDLYNKINLRQEN 178
 DB 136 SPEKLRNLEGRIDRSVNRIRSKKNELLFAELIDYQKR-----EVDLHN-----DNQ 181

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OY 179 ELKTKTYEFG-----PSGVNRE-----SPTPFNAVEVRDPRVQLESLTPQ 222
Db 182 LIRAKIAENBRNPNSSMLPBGSGNSNIEQIMPPOTOPQPF-----DSRNYFOVAL-Q 232
OY 223 QNNIEPSTA---PKIGLOLI 239
Db 233 PNNHHYSSAGREDQTAOLQV 252

RESULT 6
AG_PETHY STANDARD: PRT: 242 AA.
AC Q40885;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE AGAMOUS protein (PMAD3).
GN AG1 OR MAD3.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Asteridae; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=flower.
RX MEDLINE=94004017; PubMed=8104573;
RA Tsuchimoto S., van der Kroij A.R., Chua N.H.;
RA "Ecotypic expression of PMAD3 in transgenic petunia phenocopies the
RL petunia blind mutant.";
RL Plant Cell 5:843-853(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Mitchell;
RA Takatsui H., Kapoor M.;
RA "Silencing of PMAD3 affects floral organ and meristem identity in
RL petunia.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC -! FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -! TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN STAMENS AND CARPELS.
CC -! SIMILARITY: BELONGS TO THE MAD3 DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -! SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
CC SRP-TYPE TRANSCRIPTION FACTORS (K-BOX).
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: X72912; CAA51417.1; -.
DR EMBL: AB076051; BAB79434.1; -.
DR HSSP: P11746; 1MMN.
DR TRANSFAC: T03135; -.
DR Mendel; 9809; PETHY;MADS:8.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TE; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
FT DOMAIN 19 73 MADS.
FT 112 184 K-BOX

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SQ	SEQUENCE	242 AA;	27907 MW;	A5249306807A6BD	CRC64;
	Query Match	34.3%;	Score 417.5;	DB 1;	Length 242;
	Best Local Similarity	39.7%;	Pred. No. 5e-21;		
	Matches 96;	Conservative 50;	Mismatches 73;	Indels 23;	Caps
OY	1 MGRGIVIRIDINSTRPVTFPSKRRNGIFFKAKELATLDCAEVGLVFSSGRUYEVSST	60			
Dd	17 LGRGIEITKRLENTNTRVYTCKRRRNLKKAYELSVLCDAEVALLVFSSGRUYETANN	76			
OY	61 SRSYVIDRYGAKEEQO--VVANPSELKEMOREAASLRQOLHNLOENFYOLTGDIDLSC	117			
Dd	77 SYKATIEERYKACSSSNTSGISIAEANAO--YYOOEASKTRAQIGNLONNNRFLGESIAA	134			
OY	118 LNVEKLOSLLENOLFESLGGVRAKKDHILLIDHILNKRASLFHOENDVLNKKILTMOEN	177			
Dd	135 LNLRLRLNEOKTIEGISKIRAKNELLEFAEIEYMOKR-----ETDLHN-----NN	180			
OY	178 DELHKRIKETEGPGGVNRESPTPENFAYV---ETRDPVVOLETSTLPQQUNNIESTAPKL	234			
Dd	181 QYLRAKIAIETERSOOMNL-MFGSSSYDLYVPQGSFDARANYLGVAQLGTNNHHYPRQDDPL	239			
OY	235 GL 236				
Dd	240 QL 241				

```

RESULT 7
AGL5_ARATH
ID AGL5_ARATH STANDARD: PRT: 246 AA.
AC P29385;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Agamous-like MADS box protein AGL5.
GN AGL5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RT homeotic and transcription factor genes."
RL Genes Dev. 5:484-495(1991)
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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CC -----
DR EMBL, M55553, AAA32735.1; -.
DR PIR, E39534, E39534.
DR HSSP, P11746, 1NNM.
DR TRANSFAC, T03028; -.
DR InterPro, IPR002487; K-box.
DR InterPro, IPR002100; MADS-box.
DR Pfam, PF01486; K-box; 1.
DR Pfam, PF00319; SRF-TF; 1.
DR PRINTS, PR00404; MADSDOMAIN.
DR

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Query Match	Best local	Similarity	Score	DB 1	Length	248
Matches	96	Conservative	49	Mismatches	69	Indels
1	MGRGKIVIRINDINSTSRVTFSKRRNGIFKKAKELALICDAEVLGIVFSSTGLREYSSST	60				
17	IGRGKIEIKRIGENTNTNRQVTFCKRRRGLLKKAYELSLVLCDAEVALVFSNRRLLEYANN	76				
61	SKMSYIDRKAKKEEQ---VYANNSSEIKFMOREASLRQOLHNUQENYRQLTGDDLSG	117				
77	SVKATIERKPKKCSOSSNTGSVSEANAQ---YYQEQASKLRADIGNLMNORNMGBALAG	134				
118	LWKELOSIFENDELTLGCVRAKKHLLIDELTHIDNRKASLFEHOENTDLNKRINILROEN	177				
135	MLKELKLNLEQKILKENGISIKRSKKNLLFLAELEYQKR-----EVDLHN-----NN	180				
178	DELHKKIYETE-----GPSGVNRESPPFFNFVAFVETRDYVQLESLTPQO	223				
181	QYLKRIATETEAHOHQOQMINLPSSSNVYHELVPPOQF---DTRN---YLQVNLQTN	234				
224	NNIEPSTARKGL	236				
235	NHPRQDPPIQL	247				
248	AA: 28723 MW: E9FDD8DF08ABF1E5 CRC64:					

OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91160981; PubMed=1672119;
 RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
 RT "AG1L-AGL, an Arabidopsis gene family with similarity to floral
 RL homeotic and transcription factor genes.";
 RN Genes Dev. 5:484-495(1991).
 RP [2]
 RC SEQUENCE FROM N.A.
 RX STRAIN=CV. COLUMBIA;
 MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,
 RA Faltmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
 RA Delany M., Boutry M., Griuell L.A., Macho R., Puigdomenech P.,
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Catolico L., Weissbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wulbach E., Drzonek H., Erle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nakamura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
 RA Reichelt J., Scharte M., Schoen O., Barges M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Hlauro C., Purnelle B., Masny D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argilou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Wals A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldblum T.V.,
 RA Priess D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuo A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shimpo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RL thaliana.";
 RN Nature 408:820-822(2000).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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 CC -----
 DR EMBL: M55550; AAA32730.1;
 DR EMBL: AL353032; CAB88295.1;
 DR PIR: A39534; A39534.
 DR HSP: P11746; 1NM.
 DR TRANSFAC: T03022;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADS00404.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00350; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 18 72 MADS.
 FT DOMAIN 111 183 K-BOX.
 SQ SEQUENCE 248 AA: 28336 MW: D377C47F231F2099 CRC64;

Query Match 33.3%; Score 405; DB 1; Length 248;
 Best Local Similarity 43.9%; Pred. No. 3,4e-20;
 Matches 90; Conservative 42; Mismatches 55; Indels 18; Gaps 5;
 QY 1 MGRKTYIRIDNSTSPQVFEKRNQIFPKAKELALICDAEGLVIFSTGRVYSST 60
 Db 16 LGKRIKRIKRIENTNÖVFCRRNGLLKAKAYELSLCDAEVALVIFSTGRVYANN 75
 QY 61 SMKSVIDRYGKAKEEDQVAVNPNS---ELKFWREPAASLRQOLNMQENRYQLTGDDLS 116
 Db 76 SVNGTIRRYKACSD--AVNPVSVEANQYQGSASLRRQIRIQSNRHVIGESLG 132
 QY 117 GLVKELOSLENQLESLKRVYAKKHLIDELHIDLNKASLPHQENTLYNKI----- 170
 Db 133 SLNFKELKNLEGRLEKIGISRVRSKKNELLVALELYMQRKEMELOHNNMVRKAKIAGARL 192
 QY 171 NLIRQENDELH-KRIYETEGSGVN 194
 Db 193 NPDQESSVIGCTTYE----SGVS 213
 RESULT 12
 ID AG1L-ARATH STANDARD: PRT: 242 AA.
 AC 038876;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Agamous-like MADS box protein AG1L.
 GN AG1L OR AT5G60910 OR MSJ3.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=96093419; PubMed=8535133;
 RA Mandel M.A., Yanofsky M.F.;
 RT "The Arabidopsis AG1L MADS box gene is expressed in inflorescence
 RL meristems and is negatively regulated by APETALA1.";
 RL Plant Cell 7:1763-1771(1995).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=98162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneo T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned P1 clones.";
 RL DNA Res. 4:401-414(1997).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- DEVELOPMENTAL STAGE: DRAMATICALLY UP-REGULATED UPON THE TRANSITION
 CC FROM VEGETATIVE TO REPRODUCTIVE DEVELOPMENT, WHERE ITS EXPRESSION
 CC IS DETECTED IN CAULINE LEAVES, STEMS, AND IN FLOWERS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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 CC -----
 CC EMBL: X60757; CAA43169.1; -
 CC HSSP: P11831; 1SRS.
 CC TRANSFAC: T03186; -
 CC InterPro: IPR002487; K-box.
 CC Pfam: PF001486; K-box; 1.
 CC PRINTS: PR00404; MADS-DOMAIN.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Nuclear protein.
 CC KW DOMAIN 3 57 MADS.
 CC FT DOMAIN 97 169 K-BOX.
 CC SQ SEQUENCE 227 AA; 26403 MW; 4976195B3BDE53F5 CRC64;

Query Match 31.8%; Score 386.5; DB 1; Length 227;
 Best Local Similarity 36.8%; Pred. No. 5; Le-19;
 Matches 81; Conservative 58; Mismatches 58; Indels 23; Gaps 5;

QY 1 MGRKIVIRIDNSTSRQVTFPSKRRNGIFPKAKELALICDAEVLGVFFSGTGLYEVSST 60
 DB 1 MGRGVOLKIRENKINQVTFPSKRRSGILKKAHEISVLCDAEVLGVFFSGTGLYEVSST 60
 QY 61 S-MKSVLDIRYGR-AKEEDQVAVANPNSSEIKFQREASLSRQOLHNLQENTYRLTGDDLSGL 118
 DB 61 S-MKSVLDIRYGR-AKEEDQVAVANPNSSEIKFQREASLSRQOLHNLQENTYRLTGDDLSGL 118
 QY 119 NKEVLOSTENOLETSLRGVRAKKDHLIDELHDLNRKASLPHQENTDLYNKINLIREND 178
 DB 121 SMKELOINLEHOLDALKHIRSKRNQLM-----HESIVLQKKRDLQEDNN 166
 QY 179 ELHKIYETEGP-----SGVNRES---PFPNFAVETRDV 211
 DB 167 QLSKKVKEKREKSAQOISGINSSSLFAHTDFLGTYSTNV 206

RESULT 15
 JOIN_LYCES
 ID JOIN_LYCES STANDARD; PRT; 265 AA.
 AC Q9FUT6;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE MADS-box JOINTLESS protein (LemDS).
 GN J
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 CX NCBI_Taxid=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Heinz 1706;
 RX MEDLINE=20426111; PubMed=10972295;
 RA Mao L., Begum D., Chuang H.W., Budiman M.A., Szymkowiak E.J.,
 RA Irish E.F., Wing R.A.;
 RT "JOINTLESS is a MADS-box gene controlling tomato flower abscission
 RT zone development.";
 RL Nature 406:910-913(2000).
 CC -1- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR THAT COORDINATES GENE

CC EXPRESSION UNDERLYING THE DIFFERENTIATION OF THE PEDICEL
 CC ABSCISSION ZONE. MAY ALSO BE INVOLVED IN THE MAINTENANCE OF THE
 CC INFLORESCENCE MERISTEM STATE.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN SHOOT
 CC TIPS AND AXILLARY BUDS. ALSO FOUND IN FULLY DEVELOPED PEDICELS AND
 CC FLOWERS.
 CC -1- BIOTECHNOLOGY: Mutation in 'JOINTLESS' yields 'stemless' tomato
 CC fruits which are widely used in the processing tomato industry.
 CC The fruits support mechanical harvesting and are not subject to
 CC physical wounding during transportation.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 PROBABLE DIMERIZATION DOMAIN FOUND IN SRF-
 CC TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL: AF275345; AAC09811.1; -
 CC InterPro: IPR002487; K-box.
 CC InterPro: IPR002100; MADS-box.
 CC Pfam: PF01486; K-box; 1.
 CC PRINTS: PR00404; MADS-DOMAIN.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Developmental protein;
 CC KW Nuclear protein.
 CC FT DOMAIN 3 57 MADS.
 CC FT DOMAIN 59 173 K-BOX.
 CC FT DOMAIN 58 61 POLY-SER.
 CC FT DOMAIN 176 183 POLY-ASN.
 CC FT DOMAIN 200 204 POLY-ASN.
 CC SQ SEQUENCE 265 AA; 30426 MW; EB687F9DD9C1B5D CRC64;

Query Match 31.7%; Score 386; DB 1; Length 265;
 Best Local Similarity 37.5%; Pred. No. 6; Le-19;
 Matches 96; Conservative 45; Mismatches 77; Indels 38; Gaps 6;

QY 1 MGRKIVIRIDNSTSRQVTFPSKRRNGIFPKAKELALICDAEVLGVFFSGTGLYEVSST 60
 DB 1 MAREKIQIKKIDNSTARQVTFPSKRRNGIFPKAKELSVLCDAVALLIFSSGKLDYSSS 60
 QY 61 S-MKSVLDIRYGR-AKEEDQVAVANPNSSEIKF-----WQREASLSRQOLHNLQENTYRLTGDDLSGL 115
 DB 61 S-MKSVLDIRYGR-AKEEDQVAVANPNSSEIKF-----WQREASLSRQOLHNLQENTYRLTGDDLSGL 115
 QY 116 SGLNVELOSTENOLETSLRGVRAKKDHLIDELHDLNRKASLPHQENTDLYNKINLIREND 175
 DB 117 OGLNIELOSTENOLETSLRGVRAKKDHLIDELHDLNRKASLPHQENTDLYNKINLIREND 176
 QY 176 END-----ELHKIYETEGP-----GPGVNRESPT--PFPNFAVETRDVQLESTL 220
 DB 177 NNNNNNNGRGAGVAVFEEEDNGFNNNNNNEDGSSSEVTPNCST-----DP 222
 QY 221 PQQNIEPTAPKLG 236
 DB 223 PQQDDSSDTSKLG 238

Search completed: August 11, 2002, 09:45:11
 Job time: 502 sec